

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 11:49:29 ; Search time 9086 Seconds
(without alignments)
12574.588 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggcgcgtgaccgaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estci:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssi:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.2	23.0	1049	12	BM457033
2	793.4	20.7	835	14	CA310925
3	780.6	20.4	935	13	BQ069145
4	761.6	19.9	973	13	BQ879837

5	743.8	19.4	781	14	CB956370
6	730.8	19.1	789	14	CA444761
7	727.4	19.0	931	13	BU527114
8	701.8	18.3	906	13	BU171407
9	699.8	18.3	983	10	BE795637
10	697	18.2	2726	11	AK048725
11	696.4	18.2	785	14	CB960090
12	695.4	18.2	851	12	BG703589
13	690.2	18.0	768	9	AL554421
14	662.4	17.3	664	12	BM722392
15	657.4	17.2	922	14	CA984031
16	654.2	17.1	682	14	CA309985
17	645.2	16.9	766	13	BU612412
18	641.6	16.8	841	14	CF995034
19	634	16.6	634	12	BQ018441
20	632	16.5	632	12	BM994326
21	632	16.5	632	12	BM994326
22	600.2	15.7	763	12	BM946923
23	592.2	15.5	628	9	AU132503
24	587	15.3	776	13	BU121855
25	578.8	15.1	1018	13	BQ723205
26	568.2	14.9	661	13	BU611033
27	565.6	14.8	823	13	BU214796
28	563.8	14.7	732	9	AL554364
29	556.2	14.5	938	13	BU553767
30	547.4	14.3	705	10	BE258134
31	538.4	14.1	910	13	BX844120
32	535.4	14.0	717	12	BM950590
33	534.8	14.0	790	13	BU117232
34	531.2	13.9	893	13	BU412532
35	529.2	13.8	543	9	AW070327
36	522.6	13.7	698	13	BU322342
37	520.4	13.6	557	9	AU154016
38	519	13.6	519	9	AL138362
39	509	13.3	510	13	BX283437
40	506.2	13.2	749	10	BF696473
41	505.6	13.2	894	14	CF617275
42	500	13.1	512	9	AI681374
43	497.8	13.0	501	9	AL138363
44	495	12.9	507	10	BE315402
45	492.4	12.9	810	14	CB960174

ALIGNMENTS

RESULT 1
BM457033
LOCUS
DEFINITION
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 1049)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12346 row: b column: 06
High quality sequence stop: 671.

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FEATURES
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        /db_xref="taxon:9606"
        /clone="IMAGE:5583269"
        /tissue_type="embryonal carcinoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_92"
        /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
        Average insert size 2.5 kb. Library enriched for
        full-length clones and constructed by Life Technologies.
        Note: this is a NIH_MGC Library."

ORIGIN
  Query Match      23.0%; Score 878.2; DB 12; Length 1049;
  Best Local Similarity 99.4%; Pred. No. 7e-121;
  Matches 902; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 2386 CAGAGCATGGCCAGTAGTTGGCAGCCGAAAGACACACAGCACCCTCTATGTCCCATGG 2445
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QY 2446 CCTAAGACTTACCCTGACCAAGCTAGTAGTGGGCCATTTACCTTGACCCAGTCCACA 2505
DB 61 CCTAAGACTTACCCTGACCAAGCTAGTAGTGGGCCATTTACCTTGACCCAGTCCACA 120
QY 2506 GTGCTCAGAGTAGTACCTGCTCTAGGGTTGCTTGAGAGGCAACCTCTCTGCGACACCCC 2565
DB 121 GTGCTCAGAGTAGTACCTGCTCTAGGGTTGCTTGAGAGGCAACCTCTCTGCGACACCCC 180
QY 2566 CACACCAAGAACTATATGTGCTTCTACTTCTCCACTGATCTGCTGGTCAGTGTATGATGCT 2625
DB 181 CACACCAAGAACTATATGTGCTTCTACTTCTCCACTGATCTGCTGGTCAGTGTATGATGCT 240
QY 2626 GTGGCCTGTGCAAGGCACTGCTAGTTCAGTCCACACATATAGTCATGTGCGACCACT 2685
DB 241 GTGGCCTGTGCAAGGCACTGCTAGTTCAGTCCACACATATAGTCATGTGCGACCACT 300
QY 2686 TCCTGCCACAGGCGGAGGAGCAGGGTGAGGGTATACCAAGCTGTATGTCAGAGCCCAT 2745
DB 301 TCCTGCCACAGGCGGAGGAGCAGGGTGAGGGTATACCAAGCTGTATGTCAGAGCCCAT 360
QY 2746 AGCCTAAAGCAACTGACAGGACAGCCTCCCTGGATGATGATGATGATGATGATGATGATG 2805
DB 361 AGCCTAAAGCAACTGACAGGACAGCCTCCCTGGATGATGATGATGATGATGATGATGATG 420
QY 2806 ACAAGAGTCCAGCAACCCCTCTTACGACAGGCTCTGTGACTGTAGGCTGCGAGGAGGC 2865
DB 421 ACAAGAGTCCAGCAACCCCTCTTACGACAGGCTCTGTGACTGTAGGCTGCGAGGAGGC 480
QY 2866 TTCCAGAGCAGTGTGTTGTAATTAGGACCCCAAGCACTGGGAGGGGCTCTTGGCTAGACCC 2925
DB 481 TTCCAGAGCAGTGTGTTGTAATTAGGACCCCAAGCACTGGGAGGGGCTCTTGGCTAGACCC 540
QY 2926 CTTGTGACAGTGCAGTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2985
DB 541 CTTGTGACAGTGCAGTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 2986 TAGCTGGTTTAAATAGCAAGGATTTACTACTGCGCCCTGCTGGCTGCGCAAAATTTGTTG 3045
DB 601 TAGCTGGTTTAAATAGCAAGGATTTACTACTGCGCCCTGCTGGCTGCGCAAAATTTGTTG 660
QY 3046 GAAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAGATTCATCA 3105
DB 661 GAAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAGATTCATCA 720
QY 3106 TGCTGTGTGTGACACAGGAAGGTGCCCATCTGCGAGGACCACTATGCGAGGAAGCTG 3165
DB 721 TGCTGTGTGTGACACAGGAAGGTGCCCATCTGCGAGGAGCCATATGCGAGGAAGCTG 780
QY 3166 CTGACTGCAGAACTAGGCT-CCCTCTGCCACGGTCCGTCGCCAGCAATAGATGTCCTGAG 3224
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Db 781 CTGACTGCAGAACTAGGCTCCCTCTGCCAGGTCGCTGGCAGCAATAGATGCTCTGAG 840
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DB 841 GCCTGCCCTCTCCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 900
QY 3284 TTGGGGG 3290
DB 901 TTTGGGG 907

RESULT 2
CA310925/c
LOCUS CA310925
DEFINITION UI-CF-FNO-afb-j-06-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
ACCESSION UI-CF-FNO-afb-j-06-0-UI 3', mRNA sequence.
VERSION CA310925
KEYWORDS CA310925.1 GI:24529023
SOURCE EST
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 835)
AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT 8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
  source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="UI-CF-FNO-afb-j-06-0-UI"
        /tissue_type="Human Lung Epithelial cells"
        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
        /clone_lib="UI-CF-FNO"
        /note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a
        modified polylinker; Site 1: EcoR I; Site 2: Not I;
        UI-CF-FNO is a subtracted cDNA library derived from two
        normalized Human lung epithelial cell libraries (EN1 and
        DUL) The library was subtracted according to according to
        Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
        1996. For additional information, contact:
        bento-soares@uiowa.edu
        TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
        6hr to LPS 24h
        TAG_LIB=UI-CF-FNO
        TAG_SEQ=CTGCTCAGGT"

ORIGIN
  Query Match      20.7%; Score 793.4; DB 14; Length 835;
  Best Local Similarity 99.3%; Pred. No. 3e-108;
  Matches 827; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
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JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaab3-remail.nih.gov
Tissue Procurement: ATCC
cDNA library Preparation: Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2039 row: 9 column: 20
High quality sequence stop: 708.

FEATURES
source

ORIGIN

Query Match	20.4%	Score 780.6;	DB 13;	Length 935;
Best Local Similarity	98.4%	Pred. No. 2.4e-106;		
Matches 820; Conservative	0;	Mismatches 9;	Indels 4;	Gaps 3;

Qy	1618	TCGGTCTGGGTTCTCGAAGCCCTTCAGTAGTGGCGTCACTACTGGAGAGTGGTGGCG	1677
Dβ	1	TCGGTCTGGGTTCTGAAGCCCTTCAGTAGTGGCGTCACTACTGGAGAGTGGTGGCG	60

Qy	1678	GAGAAGACCCAGTGGGTGATCGGGTCGCACACGAAGCCCGAAGCCGCAAGGCGAGCATC	1737
Dβ	61	GAGAAGACCCAGTGGGTGATCGGGTCGCACACGAAGCCCGAAGCCGCAAGGCGAGCATC	120

QY	1738	CAGATCAGCC	CAGCCGGGGTTC	CTCTGATCGTGATGCA	CGATGGCAACGATCAGC	1797
DB	121	CAGATCAGCC	CAGCCGGGGTTC	CTCTGATCGTGATGCA	CGATGGCAACGATCAGC	180

QY	1798	GCCTGACGGAGCCCTGGACGCGGGCTTAACTGCCGGACAAGCTTGACAAAGTGGGGTGTC	1857
DB	181	GCCTGACGGAGCCCTGGACGCGGGCTTAACTGCCGGACAAGCTTGACAAAGTGGGGTGTC	240

QY	1858	TTTCCTGGACTATGACCAAGGGTTGCTCATCTTCTACAAATGCTGATGACATGTCCTGGTTC	1917
DB	241	TTTCCTGGACTATGACCAAGGGTTGCTCATCTTCTACAAATGCTGATGACATGTCCTGGTTC	300

Qy	1918	TACACCTTCGCGAGAAGTTCCTGGCAAGCTCTGCTTACTTCAGCCCTGGCCAGAGC	1977
Db	301	TACACCTTCGCGAGAAGTTCCTGGCAAGCTCTGCTTACTTCAGCCCTGGCCAGAGC	360

QY	1978	CACGCCAATGGCAAGAACGTTTCAGCCGCTGCGGATCAACACCGTCCGCATCTAGTCCAGG	2037
DP	361	CACGCCAATGGGCTAAGACGTTTCAGCCGCTGCGGATCAACACCGTCCGCATCTAGTCCAGG	420

QY 2038 CAGAAGGAGACCAACACTCTCTGGGACCACTGCCACCTGCAGAGGCCCTGCCCAGGAGA 2097
 421 CACGAGGAGACCAACACTCTCTCTGGGACCACTGCCACCTGCAGAGGCCCTGCCCAGGAGA 479
 480 CACGAGGAGACCAACACTCTCTCTGGGACCACTGCCACCTGCAGAGGCCCTGCCCAGGAGA 538

[illegible]

QV 2158 TCCAGCCTCCAGTCTGTAAATGGAGGTGCATTCCCTACTTCCATAAATCTCTTCCAGC 2217

Qy	2992	GTTTAAATTAGACAAGGATTTACTACCTGGCCCTCGTGGCTTGCAAAATTTGTTGGAAGAG	3051
Db	830	GTTTAAATTAGACAAGGA-TTACTACCTGGCCCTCGT-GCTTGCAAAATGNTTGGGAAG	773
Qy	3052	CTGGAAGAAGAGACTCTGCTGAAATTTCCAGGAATCCACAGCGCCAGATTTCATCATGTCG	3111
Db	772	CTGGAGAAGCAGACTCTGCTG-ATTTCAGGAATCCAGCGCCAGATTTCATCATGTCG	714
Qy	3112	TTGTGACCAGGAAGCTGCCCCCATCTGCAAGGAAGCCACTATGCCAGAAAGCTGCTGACT	3171
Db	713	TTGTGACCAGGAAGCTGCCCCCATCTGCAAGGAAGCCACTATGCCAGAAAGCTGCTGACT	654
Qy	3172	GCAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCAAATAGATGTCCTGAGGCCTGCC	3231
Db	653	GCAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCAAATAGATGTCCTGAGGCCTGCC	594
Qy	3232	CCTCTCCCACTTCACTCAGTTGCCCAAAATCTAAATTTTTTACAAGAGATCTCTGTTTGGGGGA	3291
Db	593	CCTCTCCCACTTCACTCAGTTGCCCAAAATCTAAATTTTTTACAAGAGATCTCTGTTTGGGGGA	534
Qy	3292	ACTTAAGTCAGATCCAGAAACCTTGCGTGCAGAGGAGTCTGGGAAATGCTATTCCTCTAGA	3351
Db	533	ACTTAAGTCAGATCCAGAAACCTTGCGTGCAGAGGAGTCTGGGAAATGCTATTCCTCTAGA	474
Qy	3352	AGGAAGTTAGGTTGGGTGGAGCAGCCCACTCGCTGTTTTCTGCCACAGATCCCAATCG	3411
Db	473	AGGAAGTTAGGTTGGGTGGAGCAGCCCACTCGCTGTTTTCTGCCACAGATCCCAATCG	414
Qy	3412	TGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGAGGTGTCCTGCCCCCTTGGCTCTATC	3471
Db	413	TGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGAGGTGTCCTGCCCCCTTGGCTCTATC	354
Qy	3472	CTTGCCACAGAGTGGGAACCTGGAGGAGTGGGCTGCAAGA CTGAGCCTTAAATGTCCTCCCG	3531
Db	353	CCTGCCACAGAGTGGGAACCTGGAGGAGTGGGCTGCAAGA CTGAGCCTTAAATGTCCTCCCG	294
Qy	3532	GCCTTGACTTTTCTTTCTAGTCCTGGGGCTAGATTCTGCACATGGGGTCTCTGACACAA	3591
Db	293	GCCTTGACTTTTCTTTCTAGTCCTGGGGCTAGATTCTGCACATGGGGTCTCTGACACAA	234
Qy	3592	CACACCATCCCAAAAGTAGCCGGAAGAGCTAAACA CAGGGGGTCTTAAAAATGGCTGCCCC	3651
Db	233	CACACCATCCCAAAAGTAGCCGGAAGAGCTAAACA CAGGGGGTCTTAAAAATGGCTGCCCC	174
Qy	3652	CGCACCCGGGCTCCCTTGGGCHAAAAGGAATTTGTAGCCCTACCCCAA CCGTTCAACTA	3711
Db	173	CGCCACCCGGGCTCCCTTGGGCHAAAAGGAATTTGTAGCCCTACCCCAA CCGTTCAACTA	114
Qy	3712	CCAGAACTCTGGGCCACCCACAGCAGTATTTTTATTTAAAAATGTTGCCCATTTTATGAGTTA	3771
Db	113	CCAGAACTCTGGGCCACCCACAGCAGTATTTTTATTTAAAAATGTTGCCCATTTTATGAGTTA	54
Qy	3772	TGATCAAAATTTGATTTAAATTTAAAGTTACAGATGTCAAAAAA AAAAAA AAAAAA	3824
Db	53	TGATCAAAATTTGATTTAAATTTAAAGTTACAGATGTCAAAAAA AAAAAA AAAAAA	1

RESULT 3
BQ069145
LOCUS
DEFINITION
BQ069145 935 bp mRNA linear EST 02-APR-2002
AGENCOURT 6738796 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5803435
5', mRNA sequence.
BQ069145
BQ069145
BQ069145.1 GI:19898191
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
NIH-MGC <http://mgc.nci.nih.gov/>.
REFERENCE
AUTHORS
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
SOURCE

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCAATGC.

TAG_TISSUE=lung
TAG_LIB=UI-H-DH1
TAG_SEQ=AGATCAATGC"

ORIGIN

Query Match 19.1%; Score 730.8; DB 14; Length 769;
Best Local Similarity 99.1%; Pred. No. 6.3e-99;
Matches 735; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3076 TTCAGGAATCCAGGCGCAGATTCATCATGTCTGTGTGACAGGAAGCTGCCCCCA 3135
DB 742 TTTCCAGAACTCCAGGCGCAGATTCATCATGTCTGTGTGACAGGAAGCTGCCCCCA 683
QY 3136 TCTCAGGAAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCAC 3195
DB 682 TCTCAGGAAGCCACTATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCAC 623
QY 3196 GGTCCGTCGCCAGCAATAGATGTCTGTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCC 3255
DB 622 GGTCCGTCGCCAGCAATAGATGTCTGTGAGGCTGCCCTCTCCCACTTCACTCAGTTCCC 563
QY 3256 AATCTAAATTTTACAGAGATTCCTGTTGGGGAACTTAAGTCAGATCAGAACTTG 3315
DB 562 AATCTAAATTTTACAGAGATTCCTGTTGGGGAACTTAAGTCAGATCAGAACTTG 503
QY 3316 GCTGCAAGGAGCTGCGGAATGTCATTTCCCTAGAGGAAGTTAGGTTGGTGGACAA 3375
DB 502 GCTGCAAGGAGCTGCGGAATGTCATTTCCCTAGAGGAAGTTAGGTTGGTGGACAA 443
QY 3376 GCCCACTCGCTTTTCTGCCAGAGATCCAAATCGTGAAGAACTCGGGAGAGGGTGGAG 3435
DB 442 GCCCACTCGCTTTTCTGCCAGAGATCCAAATCGTGAAGAACTCGGGAGAGGGTGGAG 383
QY 3436 TCACATCTAGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGTGGGAACCTGGAG 3495
DB 382 TCACATCTAGGTTGTCTGCCCTTGGCTCTATCCCTGCCAGAGTGGGAACCTGGAG 323
QY 3496 GAGTGGGCTCAAGACTGAGCTTAATGTCTCCCGGCTTACTTTTCTTCTAGTCCT 3555
DB 322 GAGTGGGCTCAAGACTGAGCTTAATGTCTCCCGGCTTACTTTTCTTCTAGTCCT 263
QY 3556 GGGGCTTAGATTCGCACTTGGGCTCTTGACACACACACACATCCCAAGTAGCCGGA 3615
DB 262 GGGGCTTAGATTCGCACTTGGGCTCTTGACACACACACACATCCCAAGTAGCCGGA 203
QY 3616 GAGCTAAACACAGGGGTTCTTAAATGGCTGCCCGGCTTCCCTCCCTTGGGCA 3675
DB 202 GAGCTAAACACAGGGGTTCTTAAATGGCTGCCCGGCTTCCCTCCCTTGGGCA 143
QY 3676 AAAGGAATTCGAGCCCTACCCCAACCCCTTCAACTACAGAACTCTGGGCCACCCAGCAG 3735
DB 142 AAAGGAATTCGAGCCCTACCCCAACCCCTTCAACTACAGAACTCTGGGCCACCCAGCAG 83
QY 3736 TATTTTATTTAAATTTGGCCCAATTTATGATTAATGATTAATTAATTAAG 3795
DB 82 TATTTTATTTAAATTTGGCCCAATTTATGATTAATGATTAATTAATTAAG 23
QY 3796 TTACAGATGTCAAAAA 3817
DB 22 TTACAGAAAAA 1

RESULT 7

BUS271114

LOCUS

DEFINITION

10155963 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6536868 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BUS271114
BUS271114.1 GI:22837555
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@nih.gov
Tissue Procurement: ATCC

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2698 row: 0 column: 12
High quality sequence stop: 552.

FEATURES

source

1. .931
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536868"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site: 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 19.0%; Score 727.4; DB 13; Length 931;
Best Local Similarity 97.0%; Pred. No. 2e-98;
Matches 827; Conservative 0; Mismatches 16; Indels 10; Gaps 8;

QY 2100 GAGAGCTGAGCTCAGCCACCCGTCGACCTGAGACCTCAGGCCAGTTGTTTACCCTC 60
DB 1 GAAGAGCTGAGCTCAGCCACCCGTCGACCTGAGACCTCAGGCCAGTTGTTTACCCTC 60
QY 2160 CAGCTCCAGCTGTAATAATGGAGTTGCATTCCTTCTTAACTCTCTTCCAGCAT 2219
DB 61 CAGCTCCAGCTGTAATAATGGAGTTGCATTCCTTCTTAACTCTCTTCCAGCAT 120
QY 2220 CGATGTTCTGTAGCTCTGACCTTTGATAGGATACAGTTTGTATCCAGGATGTGACATGG 2279
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1 (bases 1 to 983)

REFERENCE AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov

Tissue Procurement: DCTD/DP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC802 row: 9 column: 05
High quality sequence stop: 791.

FEATURES source

1..983
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ORIGIN

Query Match 18.3%; Score 699.8; DB 10; Length 983;
Best Local Similarity 97.3%; Pred. No. 2.5e-94;
Matches 787; Conservative 0; Mismatches 12; Indels 10; Gaps 7;
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QY 3288 GGGAACTTAAGTCAGATCCAGAACCTTGG 3316
DB 771 GGGAACTTAAGTCAGATCCAGAACCTTGG 799
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DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone: C230023D16 product: similar to CDNA FLJ10759 F15, CLONE NT2RP3004617, WEAKLY SIMILAR TO ZINC-BINDING PROTEIN A33 [Homo sapiens], full insert sequence.
ACCESSION AK048725
VERSION AK048725.1 GI:26093070
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE 10349636
PUBMED
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
TITLE Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE 11042159
PUBMED
REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Iwata, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
AUTHORS RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
TITLE Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE 11076861
PUBMED
REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
AUTHORS Functional annotation of a full-length mouse cDNA collection
TITLE Nature 409, 685-690 (2001)
JOURNAL
MEDLINE
PUBMED
REFERENCE 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
JOURNAL
REFERENCE
AUTHORS

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2726)
Fukuda, S., Furuno, M., Hayatsu, N., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayashi, K., Ito, M., Kagawa, I., Kasukawa, T., Hori, P., Imotani, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
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ORIGIN

Query March 18.2%; Score 697; DB 11; Length 2726;
Best Local Similarity 68.2%; Pred. No. 5.5e-94;
Matches 1201; Conservative 0; Mismatches 240; Indels 320; Gaps 4;

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preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

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Query Match      18.2%; Score 696.4; DB 14; Length 785;
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VERSION BG703589.1 GI:13976072
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hausson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
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FEATURES
source

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EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (Bases 1 to 664)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cdna Library preparation: Dr. M. Bento Soares, University of Iowa

cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1. .664
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/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-800"
/notes="Organ: eye; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-800 is a cdna library containing the following
tissue(s): fetal eye. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cdna synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cdna was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cdna contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCGTATACC. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."

ORIGIN
Query Match 17.3%; Score 662.4; DB 12; Length 664;
Best Local Similarity 99.8%; Pred. No. 9.6e-89; Indels 0; Gaps 0;
Matches 663; Conservative 0; Mismatches 1;
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Db 1 AGGATCTCCGTCCTCAGCCGCTCACAGCCTCTCCAGCGCCCATCGCTTGAGCTGCC 60
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Db 421 AGGCGCAGGCGCGCGCGAGCTGCGCCGAGTCCCGCGCAGCTTCGCGAGCCCGCGTGG 480
371 CGCCAGGCTCAAGCTGGCCCAACATCTGTTGAGCGCTACAGCTCTCTCCGCTGGACGCA 850
Db 481 CGCCAGGCTCAAGCTGGCCCAACATCTGTTGAGCGCTACAGCTCTCTCCGCTGGACGCA 540
371 TCCTCAAGCGCGCGCGCGCGAGCCCTGCGAGGCGCACGACAGGTCAGGCTCTTCT 910

Search completed: July 31, 2004, 19:26:34
Job time : 9095 secs

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 00:24:56 ; Search time 14390 Seconds
(without alignments)
11524.006 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 15

Total number of hits satisfying chosen parameters: 480304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3163	82.7	3436	6	AX877131	AX877131 Sequence
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15	1695	44.3	2246	6	AX775829	AX775829 Sequence
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18	1230	32.1	2207	6	AX776017	AX776017 Sequence
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20	788	20.6	45845	6	AX491282	AX491282 Sequence
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ALIGNMENTS

RESULT 1	AX491279	AX491279	3826 bp	DNA	linear	PAT 16-AUG-2002
AX491279	LOCUS	Sequence 3 from Patent WO0212285.				
AX491279	DEFINITION	Sequence 3 from Patent WO0212285.				
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AX491279	VERSION	AX491279.1	GI:22223980			
AX491279	KEYWORDS					
AX491279	SOURCE	Homo sapiens (human)				
AX491279	ORGANISM	Homo sapiens				
AX491279	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AX491279	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AX491279	TITLE	Killary, A., Chandler, D. and Lott, S.				
AX491279	JOURNAL	The tumor suppressor car-1				
AX491279		Patent: WO 0212285-A 3 14-FEB-2002;				

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For [low] time=unseen; and DNA

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ORIGIN

Query Match 100.0%; Score 3826; DB 6; Length 3826;

Best Local Similarity 100.0%; Pred. No. 0;

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ORIGIN

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Query Match      82.7%; Score 3163; DB 6; Length 3436;  
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DB 181 TCTCTAGCGCGCCCTCTGCTCCGCGCGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTG 240  
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QY 730 GAGCGGAGGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789  
DB 361 GAGCGGAGGCGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 790 GCGCCAGCTCAAGTGGGCAACATCGTGAGCGCTACAGCTCTCTTCCGCTGAGCGCC 849  
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QY 1150 GAGGGCTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1209
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QY 2230 TAGCTCTGACTTGTATAGGATACAGCTTGTGATCCAGAGGATGTCATGCTGCTTCTCTCA 2289  
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QY	2350	GTCTCCCTCCAGCCCGACCTGCAGCTCAGNAGTGTGAGGATGSCCAGTAGTGGCAG	2409
DB	1980	GTCTCCCTCCAGCCCGACCTGCAGGAGTGTGAGGATGSCCAGTAGTGGCAG	2039
QY	2410	CCGAAAGACACACAGCACCCCTCTTATGTGCCATGGCCTAAGACTTACCCTGACCAAGC	2469
DB	2040	CCGAAAGACACACAGCACCCCTCTTATGTGCCATGGCCTAAGACTTACCCTGACCAAGC	2099
QY	2470	TAGTGATGGGCATTTACCTTTGACCCAGTCCACAGTGTGCAGGTAGTACCTGTGCTC	2529
DB	2100	TAGTGATGGGCATTTACCTTTGACCCAGTCCACAGTGTGCAGGTAGTACCTGTGCTC	2159
QY	2530	TAGGGTTGCTGAGAGCCAACTCTCTGTGCCACCCACACCAAGACTATATGGTTTCCT	2589
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QY	2590	ACTTCTCCCACTGATCTGTGGTGCAGTATGATGCTGTGGCCTGTGGAAGCACCTGGTA	2649
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QY	2770	GCCTCCCTGGATGATCGAGGTCCCAGTAGCTCTGAAACAAGAGTCCAGCCAAACCTCTTC	2829
DB	2400	GCCTCCCTGGATGATCGAGGTCCCAGTAGCTCTGAAACAAGAGTCCAGCCAAACCTCTTC	2459
QY	2830	AGCAGGCCCTGTGACCTGCTAGGTGTCAGGAGCTTCCAGAAAGCAGTTGTTGTATTA	2889
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QY	3010	TTACTACTGGCCCTGGTGGCTGTGCAAAATTTGTTGAAGAGCTGGAGAGCAGACTCTG	3069
DB	2640	TTACTACTGGCCCTGGTGGCTGTGCAAAATTTGTTGAAGAGCTGGAGAGCAGACTCTG	2699
QY	3070	CTGAATTTCCAGGAACCTCCAGGCCAGATTCACTATGCTGTGTCACCAAGAAAGCTG	3129
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QY	3130	CCCCATCTGCAGGAAGCCATATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTC	3189
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DB	2820	TGCCACGGTCCGTGCCAGCAATAGATGTCTGAGGGCTGCCCTCTCCCACTTCACTCA	2879
QY	3250	GTTTCCCAATCTAAATTTTACAAGAGATTCTGTTTGGGGGAACCTTAAGTCAGATCCAGA	3309
DB	2880	GTTTCCCAATCTAAATTTTACAAGAGATTCTGTTTGGGGGAACCTTAAGTCAGATCCAGA	2939
QY	3310	ACCTTGCTGCAAGGGAGTCTGGGAAATGTATTTCCCTTAGAGGAAGATTAGGGTGGGTG	3369
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QY	3430	GTGAGTCCACATCTAGGGTGTCTGCGCCCTTGGCTCTATCCCTGCCACAGAGTGGAA	3489
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QY	3550	AGTCTCGGGCTAGATTTCTGCATCTGGGGTCTCTGACACACACACCATCCCAAAGTAG	3609
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QY	3610	CCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGCCCCCGCACACCGGGGCTCCCT	3669
DB	3240	CCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGCCCCCGCACACCGGGGCTCCCT	3299
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DB	3300	TGGGCAAAAGGAATTTGTCAGCCCTTACCCCAACCCCTTCAAATACACAGAACTTGGGCCACCC	3359
QY	3730	CAGCAGTATTTTATTTAAATGTTGCCCATTTTATGAGTTATGATCAATTTGTATTAAA	3789
DB	3360	CAGCAGTATTTTATTTAAATGTTGCCCATTTTATGAGTTATGATCAATTTGTATTAAA	3419
QY	3790	TTAAAGTTACAGATGTC	3806
DB	3420	TTAAAGTTACAGATGTC	3436
RESULT 3			
BD156501			
LOCUS	BD156501	3436 bp	DNA linear PAT 17-JAN-2003
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD156501		
VERSION	BD156501.1	GI:27862259	
KEYWORDS	JP 2002191363-A/11344.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, I.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 11344 09-JUL-2002;		
COMMENT	HELEX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/11344 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/PC 10, PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof PH Key		
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	/db_xref="taxon:9606"	Location/Qualifiers	
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Query Match	82.7%	Score 3163;	DB 6; Length 3436;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db	61	TTCTCTCGGTACCTCTTCGGACAGCACCCCTCCCTCTCGGTAGCTCTACCC	120
Qy	490	TGCTGTGCGGGCTGCTCCGGCGCCAGCCCTCGGTCTCGACAGCGCGCG	549
Db	121	TGCTGTGCGGGCTGCTCCGGCGCCAGCCCTCGGTCTCGACAGCGCGCG	180
Qy	550	TCTCTAGCGCCCTGCTCCGGCGCCAGCCCTCGGTCTCGACAGCGCGCG	609
Db	181	TCTCTAGCGCCCTGCTCCGGCGCCAGCCCTCGGTCTCGACAGCGCGCG	240
Qy	610	TGAGGCTCAAGGAGAGTCTGCTGCTCCATCTGCTGAGCATCTACGAGCCG	669
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Qy	670	AGCTTGGGCTCGAGCACTACTTCTGCGCGCTGCTCATCGAGGCACTGGGTC	729
Db	301	AGCTTGGGCTCGAGCACTACTTCTGCGCGCTGCTCATCGAGGCACTGGGTC	360
Qy	730	GAGCGGAGGCGCGGAGTGTGCTGCTGCGCGGCTGCTGCTGCGGAGCGGCTG	789
Db	361	GAGCGGAGGCGCGGAGTGTGCTGCTGCGCGGCTGCTGCTGCGGAGCGGCTG	420
Qy	790	GCGCGGAGCTCAAGTGGGCAATCTGCTGAGGCTGCTGCTGCTGCGGAGCG	849
Db	421	GCGCGGAGCTCAAGTGGGCAATCTGCTGAGGCTGCTGCTGCTGCGGAGCG	480
Qy	850	ATCTCTCAAGCGCGCGCGGCGGAGTGTGCTGCGGAGGCTGCTGCTGCTG	909
Db	481	ATCTCTCAAGCGCGCGCGGCGGAGTGTGCTGCGGAGGCTGCTGCTGCTG	540
Qy	910	TGCTCTAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	969
Db	541	TGCTCTAGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
Qy	970	CATCAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1029
Db	601	CATCAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	660
Qy	1030	CTTCAGGCGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1089
Db	661	CTTCAGGCGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	720
Qy	1090	CAACTGGGGAGAGCAAGTCTTCAACAGAGCTGCGGAGCTATCGGAGGCTTC	1149
Db	721	CAACTGGGGAGAGCAAGTCTTCAACAGAGCTGCGGAGCTATCGGAGGCTTC	780
Qy	1150	GAGGGGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1209
Db	781	GAGGGGTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
Qy	1210	GACAGCGCGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1269
Db	841	GACAGCGCGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	900
Qy	1270	CGAAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1329
Db	901	CGAAGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	960
Qy	1330	ACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1389
Db	961	ACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
Qy	1390	AACCTCATATGAGACTTCCGAGCTTCAAGGTACAGAGGCGGCTCGAGTAC	1449
Db	1021	AACCTCATATGAGACTTCCGAGCTTCAAGGTACAGAGGCGGCTCGAGTAC	1080
Qy	1450	TGGAAGTCCCTGTTCCAGGACATCCACCTAGTCCAGCGGCTTAAACCTTGG	1509
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Qy	1510	ACAGCCACAGCGGCTGATCTCTCGGACAGCTGACCTTGTGGTTCAGGCAACT	1569
Db	1141	ACAGCCACAGCGGCTGATCTCTCGGACAGCTGACCTTGTGGTTCAGGCAACT	1200
Qy	1570	CACCCACAGCACTGCGAGGCTTCCGAAAGCGCTTCCGATGAGGCTGCTGGT	1629
Db	1201	CACCCACAGCACTGCGAGGCTTCCGAAAGCGCTTCCGATGAGGCTGCTGGT	1260
Qy	1630	TCTGAAGCTTCAGTGTGGGCTCCTACTTGGGAGGCTGCTGGGAGGAGGAG	1689
Db	1261	TCTGAAGCTTCAGTGTGGGCTCCTACTTGGGAGGCTGCTGGGAGGAGGAG	1320
Qy	1690	TGGGTGATCGGGCTGGGACACGAGCGCAAGCGGCAAGGCGGCTCCAGATCC	1749
Db	1321	TGGGTGATCGGGCTGGGACACGAGCGGCAAGCGGCTCCAGATCCAGATCC	1380
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Qy	1930	GAGAACTTCCCTGGCAAGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1989
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Qy	2110	ACTCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2169
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Qy	2170	TCTGAAATGGAGGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2229
Db	1800	TCTGAAATGGAGGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1859
Qy	2230	TAGCTCTGACCTTGATAGGATACAGCTTTCATCAAGGATGATGATGATGAT	2289
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Qy	2350	GTCTCCCTCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2409
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Qy	2410	CCGAAAGACACACAGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	2469
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RESULT 4
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to ZINC-BINDING PROTEIN A33.
ACCESSION
AK001621
VERSION
AK001621.1 GI:7022986
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Isogai, T., Ota, T., Hayaishi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K.,
Tanai, H., Kimata, M., Watanabe, M., Hiroaka, S., Ishii, S., Kawai, Y.,
Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K.,
Masuo, Y. and Kanehori, K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3436)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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ORIGIN

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ACCESSION		Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone	
VERSION		MGC:938 IMAGE:355572), complete cds.	
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AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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		Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zebard,C., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Casavant,T.L., Abramson,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Brancioni,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Ia,X., Gibbs,R.A., Fahey,J., Heiton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.C., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
		2388257	
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		2 (bases 1 to 3259)	
		Strausberg,R.	
		Direct Submission	
		Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
		NIH-MGC Project URL: http://mgc.nci.nih.gov	
		Contact: MGC help desk	
		Email: cgapsb@mail.nih.gov	
		Tissue Procurement: ATCC	
		cDNA Library Preparation: Rubin Laboratory	
		DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
		cDNA Sequencing by: Genome Sequence Centre.	
REMARK			
COMMENT			

```

BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: J Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 8922647.

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ORIGIN
Query Match      78.8%; Score 3014; DB 9; Length 3259;
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3811 AAAAAAAAAAAAAAAAAA 3826
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RESULT 6

BC007999

LOCUS

DEFINITION

Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone

MGC:15757 IMAGE:3357436), complete cds.

ACCESSION

BC007999

VERSION

BC007999.1

KEYWORDS

MGC.

3259 bp mRNA linear PRI 03-OCT-2003
Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone
MGC:15757 IMAGE:3357436), complete cds.
BC007999
BC007999.1 GI:14124949
MGC.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1. (bases 1 to 3259)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, K.S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22389257
PUBMED	12477932
REFERENCE	2. (bases 1 to 3259)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalios, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IPAL Plate: 23 Row: a Column: 20. Location/Qualifiers 1..3259 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:15757 IMAGE:3357436" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH_MGC_16" /lab_host="DH10B-R" /note="Vector: pOTB7" 1..3259 /gene="FLJ10759" /db_xref="LocusID:55223" 34..1461 /codon_start=1 /product="hypothetical protein FLJ10759" /protein_id="AAH07999.1"

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QY	1291	CAGATCTCGAGAGCGCTGGCTGAACCGACCGGCACACTTCTCTGGCTGGGGTGGCC	1350
Db	721	CAGATCTCGAGAGCGCTGGCTGAACCGACCGGCACACTTCTCTGGCTGGGGTGGCC	780
QY	1351	TCACGTCCGAGCGGCTCAAGGGAAATAATCCATGAGACCAACTTCAATATGAAGACTTC	1410
Db	781	TCACGTCCGAGCGGCTCAAGGGAAATAATCCATGAGACCAACTTCAATATGAAGACTTC	840
QY	1411	CCGACCTCCAAGTACACAGGCCCCCTGCAGTACCACTCTGGAAGTCCCTGTTCCAGGAC	1470
Db	841	CCGACCTCCAAGTACACAGGCCCCCTGCAGTACCACTCTGGAAGTCCCTGTTCCAGGAC	900
QY	1471	ATCCACCCAGTGCAGCGCCCTTAACCTTGACCCGGGCACAGCCCAACCAAGCGCTGATC	1530
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QY	1531	CTGTGCGAGCACTGCACATTTGTGGCTTACGGAAATTTGCCACCAAGCACTGCAGGAC	1590
Db	961	CTGTGCGAGCACTGCACATTTGTGGCTTACGGAAATTTGCCACCAAGCACTGCAGGAC	1020
QY	1591	TCGCCAAAGCCGCTTCGATGTGGAGGTGTCGGTGTGGTTCGAGCGTTTCAGTAGTGGC	1650
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QY	1651	GTCCACTACTGGGAGGTGGTGGCGGGAAGAACCCAGTGGGTGATCGGGCTGGGCACAC	1710
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QY	1771	GTGATGACGATGGCAACCAAGTACAGCGCTGCACGAGCCCTGGAGCGGCTTAACGTC	1830
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QY	1951	TGCTCTTTACTTTACGCCCTGGCCAGAGCCAGCCAAATGGCAAGAACTTCAGCGCGTGGG	2010
Db	1381	TGCTCTTTACTTTACGCCCTGGCCAGAGCCAGCCAAATGGCAAGAACTTCAGCGCGTGGG	1440
QY	2011	ATCAACACCGTCGGATCTAGTCCAGGCAAGAGACCAACCTCTGGGACCACTGC	2070
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QY	2251	TACAGCTTTTATCCAGGATGTGACATGCTTCTCTCAGGCAACCCCTGCCCACCCCT	2310
Db	1680	TACAGCTTTTATCCAGGATGTGACATGCTTCTCTCAGGCAACCCCTGCCCACCCCT	1739

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QY	2371	GACCTCAGGAAGTGTTCAGAGCATGGCCAGTAGTTGGCGAGCCGGAAGACACACAGCAACC	2430
Db	1800	GACCTCAGGAAGTGTTCAGAGCATGGCCAGTAGTTGGCGAGCCGGAAGACACACAGCA-CC	1858
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Db	2099	CATGTGCCACACCTTCTCTGCCACAGCCCGAGGGACAGGCTGAGGTATACCCAAAGCT	2158
QY	2731	GATGCAGAGCCCATTAGCCTAAAGAACTGCGAGGACAAGCTTCCCTGGATGATCGAGT	2790
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Db	2699	CAGAGATCTGTTTGGGGGAACTTAAGTCAGATCCAGAACTTGGCTGCGAAGGAGTCT	2758
QY	3331	GGGAAATGTCAATTCCTTAGAAGGAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTT	3390
Db	2759	GGGAAATGTCAATTCCTTAGAAGGAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTT	2818
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Db	2879	GTCTGCGCCCTGGCTCTATCCCTGCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGA	2938	
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QY	3571	CACCTGGGGTCTCTGACACACACACACATCCCAAGTAGCCGAGAGCTAAACACACAGG	3630	
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QY	3751	TGTTGCCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	3810	
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LOCUS	BC011689	3259 bp mRNA linear PRI 19-DEC-2003		
DEFINITION	Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone			
ACCESSION	MGC:19672 IMAGE:3353034), complete cds.			
VERSION	BC011689			
KEYWORDS	MGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 3259)			
AUTHORS	Stausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, B.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.D., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, W.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
REFERENCE	2 (bases 1 to 3259)			
AUTHORS	Stausberg, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:15079757.
Contact: MGC help desk
Email: cgaps-f@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 27 Row: b Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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	Best Local Similarity	99.9%;	Pred. No. 0;							
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QY	571	CCTCGGGCCCCCTCTCTGCTGCCCCCTGCGGCCCATGCGTGCAGCCCTCAAGACGAGCTG	630							
DB	1	CCTCGGGCCCCCTCTCTGCTGCCCCCTGCGGCCCATGCGTGCAGCCCTCAAGACGAGCTG	60							
QY	631	CTGTGCTCCATCTGCTGAGCATCTACAGAACCCGCTGAGCCTTGGGTGCGAGCATCTAC	690							
DB	61	CTGTGCTCCATCTGCTGAGCATCTACAGAACCCGCTGAGCCTTGGGTGCGAGCATCTAC	120							
QY	691	TTCTGCCCGCGCTCATCACAGGACACTGGTGGCGGAGGAGGCGCAGGGGCCCGCGAC	750							
DB	121	TTCTGCCCGCGCTCATCACAGGACACTGGTGGCGGAGGAGGCGCAGGGGCCCGCGAC	180							
QY	751	TGCCCCGAGTGCCCGGCGCACCTTCGCGGAGCCCGCTGGCGGCCAGCTCTCAAGCTCGCC	810							
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QY	811	AACATCTGAGCGCTACAGCTCTTCCCGTGTGACGCACTCTCAACGCGCGCGCGCC	870							
DB	241	AACATCTGAGCGCTACAGCTCTTCCCGTGTGACGCACTCTCAACGCGCGCGCGCC	300							
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2999	C	A	TTGGGGT	CTCTGACACACACACCATCCCAAGTAGCGGAGAGCTTAACACAGGG	3058
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3059	G	GT	TTCT	TAATAATGGCTGCCCGCCACCCCGGCCCTCCCTTGGGCAAAAGAAATGTGCAG	3118
3691	C	T	A	CCCCAACCCCTTCAACTACAGAACTCTGGGCCACCCGACAGTATTTTATTTAAA	3750
3119	C	T	A	CCCCAACCCCTTCAACTACAGAACTCTGGGCCACCCGACAGTATTTTATTTAAA	3178

QY	3751	TGTTGCCCATTTTATGAGTATGATCAATCAATTTGTTAAATTTAAAGTTTACAGATGTCAAAA	3818
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RESULT 8			
BC012152			
LOCUS			
DEFINITION	Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone		
ACCESSION	MGC:20370 IMAGE:458639), complete cds.		
VERSION	BC012152		
KEYWORDS	BC012152.1 GI:15082475		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3259)		
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Suetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Utsin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villallon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shvchenko,Y., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalski,U., Smalusi,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 3259)		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Len Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Tilisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalusi, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			

Series: IRAL Plate: 29 Row: d Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922647.

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Best Local Similarity		99.9%;	Pred. No. 0;	
Matches 3254; Conservative		0; Mismatches	0; Indels 2; Gaps 2;	
QY		571	CCTCGGGCCCCCTCTCTGCTGCGCCCTGGCGCCATGGCGTGGAGCCTCAAGGACGAGCTG 630	
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QY	871	GGCGGACCCCTGGCAGGCGCACGACAAAGGTCAAGCTCTTCTGCTCAACGACCGCGGCTT 930		
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RESULT 9

AX775831

LOCUS

DEFINITION

ACCESSION

VERSION
KEYWORDS

KEYWORDS
SOURCE

SOURCE
ORGANIZATION

1.1.5.

REFERENCE

AUTHOR
ENTRY F

TITLE

WUOL

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DB	1090	GTCCACTTACTGGAGGTGTGTGGCGGAGAACCCAGTGGGTGATCGGGCTGGCACAC	1149
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ACCESSION AK122896
VERSION AK122896.1 GI:34528340
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3148)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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DEFINITION Sequence 7 from Patent WO0212285.
ACCESSION AX491283
VERSION AX491283.1 GI:22323984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Killary,A., Chandler,D. and Lott,S.
AUTHORS The tumor suppressor car-1
TITLE Patent: WO 0212285-A 7 14-FEB-2002;
JOURNAL BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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DEFINITION Homo sapiens chromosome 1 clone RP11-150F21, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
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VERSION AC022262.4 GI-8569825
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 164950)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164950)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 16, 2000 this sequence version replaced gi:7321934.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0150F21
----- Summary Statistics -----
Sequencing vector: M13; 75%
Sequencing vector: plasmid; 25%
Chemistry: Dye-terminator ET; 75% of reads
Chemistry: Dye-terminator Big Dye; 25% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163188 bases at least Q40
Consensus quality: 163696 bases at least Q30
Consensus quality: 163935 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 164650; sum-of-contigs
Quality coverage: 7.83 in Q20 bases; agarose-fp
Quality coverage: 8.20 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 8662: contig of 8662 bp in length
* 8663 8762: gap of unknown length
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DEFINITION Sequence 8 from Patent WO0212285.				
ACCESSION AX491284				
VERSION AX491284.1 GI:23233985				
KEYWORDS Homo sapiens (human)				
SOURCE Homo sapiens				
ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE 1 Killary,A., Chandler,D. and Lott,S.				
AUTHORS The tumor suppressor car-1				
TITLE Patent: WO 0212285-A 8 14-FEB-2002;				
JOURNAL BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)				
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QY 3338 GTCAATTTCCCTAGAGGAAGTTAGGGTGGTGAGCAAGCCCAACCTTCGCTTTCTGTC 3397
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RESULT 15

AX775829

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

Sequence 99 from Patent WO03048202.

2246 bp mRNA linear PAT 14-JUL-2003

AX775829

AX775829.1 GI:32693547

Db 1747 ATCCAG 1752

Search completed: July 31, 2004, 05:57:51
Job time : 14413 secs

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us (uspto)

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2004, 23:51:46 ; Search time 1364 Seconds
(without alignments)
11916.133 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtcgctgacccgaagc.....aaaaaaaaaaaaaaaaaaaaa 3826

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 15

Total number of hits satisfying chosen parameters: 250381

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002s.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3826	100.0	3826	6	ABK12806 Human CDN
2	3163	82.7	3436	4	AHH14509 Human CDN
3	2994	78.3	3243	9	ADC37268 Nuclear f
4	2209	57.7	5858	4	Aak80624 Human imm
5	2209	57.7	22893	6	ABK12810 Human tum
6	2037	53.2	5866	4	Aak80625 Human imm
7	2037	53.2	30676	6	ABK12811 Human tum
8	1695	44.3	2246	9	ADC37266 Nuclear f
9	1230	32.1	2207	9	ADC37454 Nuclear f
10	1230	32.1	2207	9	ADC37264 Nuclear f
11	928	24.3	5858	4	Aak80626 Human imm
12	928	24.3	30625	6	ABK12808 Human tum
13	788	20.6	45845	6	ABK12809 Human tum
14	533	13.9	628	4	AHH06784 Human CDN
15	493	12.9	573	4	AHH16850 Human CDN
16	493	12.9	573	4	ABA60671 Human foe
17	493	12.9	573	4	AHH140560 Human foe
18	493	12.9	573	4	ABA28765 Probe #92
19	493	12.9	573	4	ABA28765 Probe #72
20	493	12.9	573	4	Aak34844 Human bon
21	493	12.9	573	4	Aak8953 Human bra
22	493	12.9	573	6	ABS34609 Human liv
23	431	11.3	431	4	ABS09384 Human gen
					Aai26045 Probe #15

C	24	431	11.3	431	4	ABA73209	AbA73209 Human foe
C	25	431	11.3	431	4	AAI53637	Aai53637 Probe #22
C	26	431	11.3	431	4	ABA38642	AbA38642 Probe #17
C	27	431	11.3	431	4	AAK47809	Aak47809 Human bon
C	28	431	11.3	431	4	AAK21644	Aak21644 Human bra
C	29	431	11.3	431	4	ABS47535	AbS47535 Human liv
C	30	431	11.3	431	6	ABS21816	AbS21816 Human gen
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C	32	376	9.8	2213	5	AAS90400	Aas90400 DNA encod
C	33	325	8.5	371	4	AAK61638	Aak61638 Human imm
C	34	149	3.9	49744	6	ABK12807	AbK12807 Human tum
C	35	60	1.6	60	6	ABN43449	AbN43449 Human spl
C	36	29	0.8	614	6	AEN63808	AeN63808 Human can
C	37	27	0.7	470	3	AAC59529	Aac59529 Human sec
C	38	27	0.7	189013	7	ACF62741	AcF62741 Cancer ba
C	39	27	0.7	189013	7	ADB20856	AdB20856 MRP1 base
C	40	27	0.7	189013	9	ADB87945	AdB87945 Human UGT
C	41	27	0.7	189013	9	ADB96928	AdB96928 Human MDR
C	42	27	0.7	189013	9	ADB92119	AdB92119 Human MDR
C	43	26	0.7	273	6	ABQ60500	AbQ60500 Human col
C	44	26	0.7	393	7	ABX41090	AbX41090 Bovine ES
C	45	26	0.7	411	7	ABX48150	AbX48150 Bovine ES

ALIGNMENTS

RESULT 1
ABK12806
ID ABK12806 standard; CDNA; 3826 BP.
AC ABK12806;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor CAR-1.
XX
KW Human; ss; tumour suppressor; gene; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer;
KW chromosome ip31-lp36.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 604..2031
FT /tag= a
FT /product= "CAR-1"
PT
XX WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033P.
PR 23-AUG-2000; 2000US-0227560P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Killary A, Chandler D, Lott S;
XX WPI; 2002-269088/31.
XX P-PSDB; AAU78657.
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
XX diagnosing cancer, for altering the phenotype of a tumor cell, for
XX treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Claim 2; Page 134-135; 185pp; English.

CC The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
 CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
 CC from 10-50 amino acids, an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells, a method for suppressing growth of a cancer cells by contacting
 CC the cells with the expression cassette (i.e. gene therapy), a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1
 XX
 SQ Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 U; 0 Other;

Query Match 100.0%; Score 3826; DB 6; Length 3826;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 AGGCTGGCTGGACCGAAGCGGTGGTGTAAAGTCTCGGGGGTAAAGGGTCCGCTGGG 60
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 DB 61 CAGGGTTTGGGCGGGGATCCGGGAGCTGAGGGGCGGACCCCTCTCTCTCTGTC 120
 QY 121 GGTACAGCAATGTACGGTCTGGGCTGGTGGTCCCTCCCGCAGGATTCCTCATCCCA 180
 DB 121 GGTACAGCAATGTACGGTCTGGGCTGGTGGTCCCTCCCGCAGGATTCCTCATCCCA 180
 QY 181 GCTTCTGGCCCTCCCGGACACCGGCGGATTCGACCCCTTAAGGGCTCCAC 240
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 QY 241 CCGGCTCCGGATCCCTTCTCCAGCTCTATCCCTTAGGACTGCGCCCGCCCTAGAA 300
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 QY 301 CTTCCCGCTCAGGATCTCCGTCCTCAGCCGCTCAGCCCTCTCCAGGCGCCATGCC 360
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 QY 361 TTGAGTGGCCCACTACCTCTAGACTGCTCCCGGGTGGCGTCCCGAGGAGTCTCAGCC 420
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 QY 421 GCGCAGCCCTTCTCTCGGCTTACCTCTTCCGGGACAGCACCCCTCTCTCTCGGTTAGC 480

DB 421 GCGCAGCCCTTCTCTCGGCTTACCTCTTCCGGACAGCACCCCTCTCTCTCTCGGTTAGC 480
 QY 481 TCCTTACCCCTGCTGTGGGCGCTCTCCCGCGCCAGCCCTCGGTGCTCTCTCTCGGACA 540
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 QY 541 GCGCGGCGCTCTCTCAGCGCGCCCTCTCGGCGCTCTCGGCGCCCTCTCTCTCTCGGCG 600
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 DB 601 GCCATGGCGTGCAGCTTCAAGGACGAGTGTGTCTCTCATCTGCTGCTGAGCATCTACACG 660
 QY 661 GACCCGCTGAGCTGGGCTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 DB 661 GACCCGCTGAGCTGGGCTGGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 QY 721 GTGCGGACGAGGCGCGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 DB 721 GTGCGGACGAGGCGCGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 QY 781 CCGCGCTGTGGCGCCAGCTTCAAGTGGCGCAATCTGTGGAGGCTTACAGCTCTCTCTCTCT 840
 DB 781 CCGCGCTGTGGCGCCAGCTTCAAGTGGCGCAATCTGTGGAGGCTTACAGCTCTCTCTCTCT 840
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QY 2110 ACTCCAGCCACCGTGGCCACTGGAGACCTCAGGCCAGTTGTTTACCCCTCCAGCCTCCAG 2169
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QY 2230 TAGCTCTGACCTTGATAGGATACAGCTTGTATCCAGGATGTGACATGCTTCTCTCTCA 2289
DB 1860 TAGCTCTGACCTTGATAGGATACAGCTTGTATCCAGGATGTGACATGCTTCTCTCTCA 1919
QY 2290 GGGCAACCCCTGCCCAACCCCTATCCCTATCTTCTCAGGGGCGGGGACTTACCTTCCAGT 2349
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QY 2350 GTCTCCTCCAGCCAGCCCTGACCTCAGAAAGTGTGACAGATGGCCAGTATGTTGGCAG 2409
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QY 2410 CCGGAAAGACACAGCACCTCTTATGTCCCATGGCTTAAGACTTTACCCCTGACCAAGC 2469
DB 2040 CCGGAAAGACACAGCACCTCTTATGTCCCATGGCTTAAGACTTTACCCCTGACCAAGC 2099
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DB 2100 TAGTGATGGCCATTTTACCTTTGACCCAGTCCACAGTGGTCCACAGGTAGTACCTGGTCC 2159
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QY 2650 GTTGAGTCCACACATTTAGTGTGCAACCACTTCTCTGCCCAAGGCCAGGACAG 2709
DB 2280 GTTGAGTCCACACATTTAGTGTGCAACCACTTCTCTGCCCAAGGCCAGGACAG 2339
QY 2710 GTTGAGGTTATACCCAAAGCTGATGACAGGCCCATTTAGCCTTAAAGCAACTGCAGACAA 2769
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DB 3000 GAGCAAGCCCACTCGGTTTCTGCGCAGAGATCCAACTGCTGGAAGAACTCGGAGAGG 3059
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DB 3060 GTGGAGTCCACATCTAGGCTGTCTCTGCCCTTGGCTCTATCCCTGCCAGAGTGGAA 3119
QY 3490 CTGGAGAGTGGGTGCAAGACTGAGCTTAAATGCTCTCCCGGCTTGAATTTCTTTCT 3549
DB 3120 CTGGAGAGTGGGTGCAAGACTGAGCTTAAATGCTCTCCCGGCTTGAATTTCTTTCT 3179
QY 3550 AGTCTCTGGGGCTTACATCTGACATTTGGGTCTCTGACACAACATCCCAAGTAG 3609

QY 1651 GTCCACTACTGGAGGTGGTGGTGGCGAGAGAACCCAGTGGGTGATCGGGTGGCACAC 1710
Db |||||
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QY 1711 GAAGCGGCAAGCGGCAAGGCGAGCATCCAGATCCAGCCCCAGCGGGCTTCTACTGCAATC 1770
Db |||||
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QY 1771 GTGATGCACGATGCAACACGATACAGCGCTGACAGGAGCCCTGGACGCGGGTTAAAGCTC 1830
Db |||||
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QY 1831 CGGACCAAGCTTGAACAAGTGGGTGTCTTCTGGACTATGACCAAGGCTTCTCATCTTC 1890
Db |||||
1270 CGGACCAAGCTTGAACAAGTGGGTGTCTTCTGGACTATGACCAAGGCTTCTCATCTTC 1329
QY 1891 TACAAATGCTGATGATGCTGCTGCTCTACACCTTCCGCGAGAAAGTTCCCTGGCAAGCTC 1950
Db |||||
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Db |||||
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Db |||||
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Db |||||
1569 TGGAGACCTCAGGCCAGTGTGTTACCTCCAGCCCTCAGTCTGTAAATGAGAGTTGCAT 1628
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1809 GACCTCAGGAAGTGTCCAGAGCATGGCCAGTGTGGCAGCCCGAAAGACACACAGCA-CC 1867
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QY 2551 CTCTCTGCCACCCACACCAAGAACTATATGTTTCTTCTCTCCACTGATCTGCTG 2610
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QY 2731 GATGCAGAGCCCATTTAGCCTTAAAGCAACTGCAGGACAAAGCCTCCTCGATGATCGAGGT 2790
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2288 TAGGGTGCAGGAGGCTTCCAGAGCAGTGTGTAAATTTAGGACCCCAAGCACTGGGAGGG 2347
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Db |||||
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2828 TTTGCGCACAGCATCCAAATCGTGAAGAACTCGGGAGAGGTTGGAGTCCACATCTAGGGTT 2887
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QY 3691 CCTTACCCCAACCTTCAACTACAGAACTCTGGGCCACCCAGCAGTATTTTATTTTAA 3750
Db |||||
3128 CCTTACCCCAACCTTCAACTACAGAACTCTGGGCCACCCAGCAGTATTTTATTTTAA 3187
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PR	PR	17-NOV-2000;	2000US-0249297P.
PR	PR	17-NOV-2000;	2000US-0249299P.
PR	PR	17-NOV-2000;	2000US-0249300P.
PR	PR	01-DEC-2000;	2000US-0250160P.
PR	PR	01-DEC-2000;	2000US-0250391P.

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PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 35436; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 5858 BP; 1455 A; 1579 C; 1490 G; 1334 T; 0 U; 0 Other;
XX
XX Query Match 57.7%; Score 2209; DB 4; Length 5858;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2329; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1478 CAGTGCACGCGCCCTAACCTTGGACCCGCGGCAAGCCACAGCCGCTGATCCTGTCG 1537
DB 6 CAGTGCACGCGCCCTAACCTTGGACCCGCGGCAAGCCACAGCCGCTGATCCTGTCG 65
QY 1538 ACGACTGCACCATTTGGCTTAGCGCACTTGCACCCACAGCCACTGCAGGATCGCCAA 1597
DB 66 ACGACTGCACCATTTGGCTTAGCGCACTTGCACCCACAGCCACTGCAGGATCGCCAA 125
QY 1598 AGCGCTTCGATGTGGAGGTGTGGTGTCTGAAGCCTTCAGTAGTGGGTCCACT 1657
DB 126 AGCGCTTCGATGTGGAGGTGTGGTGTCTGAAGCCTTCAGTAGTGGGTCCACT 185
QY 1658 ACTGGAGGTGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACAGAGCCG 1717
DB 186 ACTGGAGGTGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACAGAGCCG 245
QY 1718 CAAGCCGCAAGGCGACATCCAGATCCAGCCAGCCGCGCTTCTACTGATCGTATGC 1777
DB 246 CAAGCCGCAAGGCGACATCCAGATCCAGCCAGCCGCGCTTCTACTGATCGTATGC 305
QY 1778 ACGATGGCAACAGTACAGCGCTGACAGGCGCTTGGACGCGGTTCACGTCGCGGACA 1837
DB 306 ACGATGGCAACAGTACAGCGCTGACAGGCGCTTGGACGCGGTTCACGTCGCGGACA 365
QY 1838 ACGTTGACAAGTGGGTGTCTTCTGGACTATGACCAAGGCTTGCTTCATCTTCTACAATG 1897
DB

DB 366 AGCTTGACAAAGTGGGTGTCTTCTTGACACTATGACCAAGGTTGCTCATCTTCTACAAATG 425
QY 1898 CTGATGACATGTCTCTGGCTCTACACCTTCCGCGAGAAAGTTTCCCTGGCAAGCTCTGCTCTTT 1957
DB 426 CTGATGACATGTCTCTGGCTCTACACCTTCCGCGAGAAAGTTTCCCTGGCAAGCTCTGCTCTTT 485
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DB 486 ACTTCAGCCCTTGGCCAGAGCAGCCCAATGCGAAGAAAGTTTCAGCCGCTGGGATCAACA 545
QY 2018 CCGTCCGCACTAGTCCAGGACAGAGACCAACCTCTCTGGGACCACTGCCACCTGC 2077
DB 546 CCGTCCGCACTAGTCCAGGACAGAGACCAACCTCTCTGGGACCACTGCCACCTGC 605
QY 2078 AAGAGCCCTGCCAGGAAGATAGAAGACCTTGGACTCCAGCCCACTGGGACCTGGAGAC 2137
DB 606 AAGAGCCCTGCCAGG - AGATAGAAGACCTTGGACTCCAGCCCACTGGGACCTGGAGAC 664
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DB 665 CTGAGCCAGTGTGTGTACCCCTCCAGCTCCAGTCTGTAATGAGGTTGATTCCTTAC 724
QY 2198 TTCTTAACTCTCTTCCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCT 2257
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DB 785 TTGATCCAGGATGTGACATGGCTTCTCTCAGGCAACCCCTGCCCAACCCCTCATCCCC 844
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DB 845 ATCTTCTCAGGCGCAGGAGACCTTCCAGTGTCTCCCTCAGCCAGCCCTGACCTCA 904
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QY 2438 TCCCATGGCTTAAGACTTACCCTTGACCAAGCTAGTGTGGGCCATTTACCTTTGACCCCC 2497
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DB 1025 AGTCCACAGTGTGTCAGAGTACCTGCTCTAGGTTGCTCAGAGCCCACTCTCT 1084
QY 2558 GCCACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2617
DB 1085 GCCACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1144
QY 2618 ATGATGCTGTGGCTGTGGAAGGACCTGGTAGTTGAGTCCACATTAATGATGTGC 2677
DB 1145 ATGATGCTGTGGCTGTGGAAGGACCTGGTAGTTGAGTCCACATTAATGATGTGC 1204
QY 2678 CACCACTTCTTCTGCCACAGGCGGAGGAGGATACCCAAAGCTGATGTCAG 2737
DB 1205 CACCACTTCTTCTGCCACAGGCGGAGGAGGATACCCAAAGCTGATGTCAG 1264
QY 2738 AGCCCATTAGCCCTAAAGCAACTGAGGACAAAGCTTCCCTGGATGATCGAGGTCCCACT 2797
DB 1265 AGCCCATTAGCCCTAAAGCAACTGAGGACAAAGCTTCCCTGGATGATCGAGGTCCCACT 1324
QY 2798 AGCTCTGAACAAGTCCAGCCAAACCTTCTTCCAGCCAGCCCTCTGTGACCTGTAGGGTG 2857
DB 1325 AGCTCTGAACAAGTCCAGCCAAACCTTCTTCCAGCCAGCCCTCTGTGACCTGTAGGGTG 1384
QY 2858 CAGGAGGCTTCCAGAGCAGTGTGTAATAGGACCCAGACCTGGGAGGGGCTGTGG 2917
DB 1385 CAGGAGGCTTCCAGAGCAGTGTGTAATAGGACCCAGACCTGGGAGGGGCTGTGG 1444
QY 2918 CTAGACCCCTTGTGACACTTGGCACTATCTCAGTGTAGGATCCTGTCAGAAAAACAAGA 2977
DB 1445 CTAGACCCCTTGTGACACTTGGCACTATCTCAGTGTAGGATCCTGTCAGAAAAACAAGA 1504

57.7%	Score 2209;	DB 6;	Length 22893;
100.0%	Pred. No. 0;		
Conservative 2329;	Mismatches 0;	Indels 1;	Gaps 1;

QY	1478	CAGTGCACGCGCGCCTTAACCTGTGACCGCGGCA	CAGCCCAAGCCGCTGATCCTGTGCG	1537
DB	11989	CAGTGCACGCGCGCCTTAACCTGTGACCGCGGCA	CAGCCCAAGCCGCTGATCCTGTGCG	12048
QY	1538	ACGACTGCACCATTTGTGGCTTACCGCAACTTGAC	CCACACCACTGCAGACTGCGCAA	1597
DB	12049	ACGACTGCACCATTTGTGGCTTACCGCAACTTGCA	CCACACCACTGCAGACTGCGCAA	12108
QY	1598	AGCCGCTTCGATGTGGAGGTGCGGTGCTGGGTTCT	GAAAGCCTTCAGTGTGGGTCGCACT	1657
DB	12109	AGCCGCTTCGATGTGGAGGTGCGGTGCTGGGTTCT	GAAAGCCTTCAGTGTGGGTCGCACT	12168
QY	1658	ACTGGGAGGTGGTGGTGGCGGAGGAACCCAGTGGG	TGATCGGCGCTGGGCACACGAAGCCG	1717
DB	12169	ACTGGGAGGTGGTGGTGGCGGAGGAACCCAGTGGG	TGATCGGCGCTGGGCACACGAAGCCG	12228
QY	1718	CAAGCCCAAGGCGAGCATCCAGATCCAGCCACGCG	CGGCTTCTACTGATCGTATGC	1777
DB	12229	CAAGCCCAAGGCGAGCATCCAGATCCAGCCACGCG	CGGCTTCTACTGATCGTATGC	12288
QY	1778	ACGATGGCAACAGTACAGGCGCTTGACGAGCGCCT	TGGACCGGCTTAAAGTCGCGGAC	1837
DB	12289	ACGATGGCAACAGTACAGGCGCTTGACGAGCGCCT	TGGACCGGCTTAAAGTCGCGGAC	12348
QY	1838	AGCTTGACAGGTGGGTGCTTCTCTGACTATGACCA	AGGCTTGCTCATCTTCTCAATG	1897
DB	12349	AGCTTGACAGGTGGGTGCTTCTCTGACTATGACCA	AGGCTTGCTCATCTTCTCAATG	12408
QY	1898	CTGATGACATGCTCTGTGCTCTACCTTCGCGAGAG	ATTCCTTGGCAAGCTCTGCTTT	1957
DB	12409	CTGATGACATGCTCTGTGCTCTACCTTCGCGAGAG	ATTCCTTGGCAAGCTCTGCTTT	12468
QY	1958	ACTTCAGCCCTGGCGAGGACAGCCCAATGGCAAGA	ACGTTTACGCCGCTGCGGATCAACA	2017
DB	12469	ACTTCAGCCCTGGCGAGGACAGCCCAATGGCAAGA	ACGTTTACGCCGCTGCGGATCAACA	12528
QY	2018	CCGTGCGCATCTAGTCCAGGCAAGAGAGACCAAC	ACCTCTCTGGGACCACTGCCACCTGC	2077
DB	12529	CCGTGCGCATCTAGTCCAGGCAAGAGAGACCAAC	ACCTCTCTGGGACCACTGCCACCTGC	12588
QY	2078	AAGAGCCCTGCCAGGAGATAGAACCTTGGACTCC	AGCCCAACCGTGGCGCACTGGAGAC	2137
DB	12589	AAGAGCCCTGCCAGG-AGATAGAAGACCTTGGACT	CCAGCCCAACCGTGGCGCACTGGAGAC	12647
QY	2138	CTCAGGCCAGTGTGTTTACCTCCAGCGCTCCAGTCT	GTAATGGAAGTTGCCATCCCTAC	2197
DB	12648	CTCAGGCCAGTGTGTTTACCTCCAGCGCTCCAGTCT	GTAATGGAAGTTGCCATCCCTAC	12707
QY	2198	TTCTTAAACTCTCTCCAGCATCGATGTTCTGTPAG	CTCTGACCTTGATAGGATACAGCT	2257
DB	12708	TTCTTAAACTCTCTCCAGCATCGATGTTCTGTPAG	CTCTGACCTTGATAGGATACAGCT	12767
QY	2258	TTGATCCAGAGATGTGACATGGCTTCTCTCAGGCA	ACCCCTGCCCAACCTCATCCCC	2317
DB	12768	TTGATCCAGAGATGTGACATGGCTTCTCTCAGGCA	ACCCCTGCCCAACCTCATCCCC	12827
QY	2318	ATCTTCTCAGGGGACGGGACTACCTTCCAGTGTCT	CTCCCTCCAGCCCAAGCCCTGACCTCA	2377
DB	12828	ATCTTCTCAGGGGACGGGACTACCTTCCAGTGTCT	CTCCCTCCAGCCCAAGCCCTGACCTCA	12887
QY	2378	GGAAGTGTCCAGAGCATGGCCAGTGTGGACGCCG	GAAGAACAACAGCACAGCACCCCTCTTATG	2437
DB	12888	GGAAGTGTCCAGAGCATGGCCAGTGTGGACGCCG	GAAGAACAACAGCACAGCACCCCTCTTATG	12947
QY	2438	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAG	TGATGGGCCATTTACCTTGACCCC	2497
DB	12948	TCCCATGGCTTAAGACTTACCCCTGACCAAGCTAG	TGATGGGCCATTTACCTTGACCCC	13007

QY 3578 GGTCTCTGACAAACACACACATCCCAAGTAGCCGAGAGCTAAACACAGGGGGTCTTT 3637
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
Db 14088 GGTCTCTGACAAACACACACATCCCAAGTAGCCGAGAGCTAAACACAGGGGGTCTTT 14147
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
QY 3638 AAAATGGCTGCCCCCGCCACCCCGGCTCCCTTTGGGCAAAAGGAATGTGAGCCCTACCC 3697
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
Db 14148 AAAATGGCTGCCCCCGCCACCCCGGCTCCCTTTGGGCAAAAGGAATGTGAGCCCTACCC 14207
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
QY 3698 CAACCCCTTCAACTACACAGAACTGCGGCCACCCACCCAGCAGTATTTTATTTAAATGTTGCC 3757
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
Db 14208 CAACCCCTTCAACTACACAGAACTGCGGCCACCCACCCAGCAGTATTTTATTTAAATGTTGCC 14267
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
QY 3758 CATTTATGAGTTATGATCAATTTGTTATTAATTAATTAATTAATGTTGCC 3807
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
Db 14268 CATTTATGAGTTATGATCAATTTGTTATTAATTAATTAATTAATGTTGCC 14317
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234274P.
PR 21-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.

RESULT 6
AAK80625
ID AAK80625 standard; DNA; 5866 BP.
XX AAK80625;
AC
XX
XX
DT 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35437.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX
XX WO200157182-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.

Db 1204 CACCACCTTCTGCCCCACAGCGGAGGAGCAGGGTGAGGGTATATCCAAAGCTGATGCAG 1263
QY 2738 AGCCCATTTAGCCTAAAGCAACTGCAGGACAAGCCTCCCTGGATGATCGAGGTCCCAAGT 2797
Db 1264 AGCCCATTTAGCCTAAAGCAACTGCAGGACAAGCCTCCCTGGATGATCGAGGTCCCAAGT 1323
QY 2798 AGCTCTGAACAAGAGTCCAGCCAAACCTCTTACAGCAGGCTCTGTACCTGTAGGGTG 2857
Db 1324 AGCTCTGAACAAGAGTCCAGCCAAACCTCTTACAGCAGGCTCTGTACCTGTAGGGTG 1383
QY 2858 CAGAGGCTTCCAGAACAGTGTGTAAATTAGACCCCAAGCACTGGAGGGGCTGTGG 2917
Db 1384 CAGAGGCTTCCAGAACAGTGTGTAAATTAGACCCCAAGCACTGGAGGGGCTGTGG 1443
QY 2918 CTAGACCCCTTGTGAGACTTGGCACTCTATCTCAGTTAGGATCTGTCTGCAGAAACAAGA 2977
Db 1444 CTGACCCCTTGTGAGACTTGGCACTCTATCTCAGTTAGGATCTGTCTGCAGAAACAAGA 1503
QY 2978 GCCATTGTAGCTGGTTTAAATTAGACAAGGATTTACTCTGGCCCTCTGGCTTGCAA 3037
Db 1504 GCCATTGTAGCTGGTTTAAATTAGACAAGGATTTACTCTGGCCCTCTGGCTTGCAA 1563
QY 3038 AATTGTTGGAAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAG 3097
Db 1564 AATTGTTGGAAGAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACCTCCAGGCCAG 1623
QY 3098 ATTCAATGCTGTGTGTGACAGGAAAGCTGCCCCATCTGCGAAGAGCCACATATGCCA 3157
Db 1624 ATTCAATGCTGTGTGTGACAGGAAAGCTGCCCCATCTGCGAAGAGCCACATATGCCA 1683
QY 3158 GAAAGCTGTGACTGACAGAACTAGGCTCTCTGCGAGGCTCCGTCAGCCCAATAGATG 3217
Db 1684 GAAAGCTGTGACTGACAGAACTAGGCTCTCTGCGAGGCTCCGTCAGCCCAATAGATG 1743
QY 3218 TCCTGAGGCTGCCCTCTCCACATCTCACTAGTTCCCAAACTAAATTTTACAGAGA 3277
Db 1744 TCCTGAGGCTGCCCTCTCCACATCTCACTAGTTCCCAAACTAAATTTTACAGAGA 1803
QY 3278 TTCTCTTTGGGGGAATTAAGTCAGATCCAGAACCTTGGCTCAGAGGAGTCTGGGAAT 3337
Db 1804 TTCTCTTTGGGGGAATTAAGTCAGATCCAGAACCTTGGCTCAGAGGAGTCTGGGAAT 1863
QY 3338 GTCAATTCCTAGAGGAAGTATGGTGGTGAGCAAGCCCACTCGGTTTCTGTC 3397
Db 1864 GTCAATTCCTAGAGGAAGTATGGTGGTGAGCAAGCCCACTCGGTTTCTGTC 1923
QY 3398 ACAGATCCAAATCGTGAAGAACTCGGAGAGGTGGAGTCCACATCTAGGGTTGTCTGC 3457
Db 1924 ACAGATCCAAATCGTGAAGAACTCGGAGAGGTGGAGTCCACATCTAGGGTTGTCTGC 1983
QY 3458 CCCTTGGCTCTATCCCTGCCCCAGAGTGGGAACTGAGAGTGGGCTGCAAGACTGAGCC 3517
Db 1984 CCCTTGGCTCTATCCCTGCCCCAGAGTGGGAACTGAGAGTGGGCTGCAAGACTGAGCC 2043
QY 3518 TAAATGTCCTCCCGGCTTCACTTTCTTCTAGTCTCTGGGCTAGATTTCTCACTTGG 3577
Db 2044 TAAATGTCCTCCCGGCTTCACTTTCTTCTAGTCTCTGGGCTAGATTTCTCACTTGG 2103
QY 3578 GGTCTCTGACACACACACCATCCAAAGTAGCGGAAAGAGCTAAACACAGGGGGTTCTT 3637
Db 2104 GGTCTCTGACACACACACCATCCAAAGTAGCGGAAAGAGCTAAACACAGGGGGTTCTT 2163
QY 3638 AAAATGSGCTGCCCGCCGCAACCGGGCTCCCTTGGGGGAAAAGGAATTTGTAGCCCTACCC 3697
Db 2164 AAAATGSGCTGCCCGCCGCAACCGGGCTCCCTTGGGGGAAAAGGAATTTGTAGCCCTACCC 2223
QY 3698 CAACCCCTTCACTACAGATCTGGGCCACCCAGCAGTATTTTAAATGTTGCC 3757
Db 2224 CAACCCCTTCACTACAGATCTGGGCCACCCAGCAGTATTTTAAATGTTGCC 2283
QY 3758 CATTTTATGATGATGATCAATTTGTTATTTAAATTAAGTTACAGATGCA 3807
Db 2284 CATTTTATGATGATGATCAATTTGTTATTTAAATTAAGTTACAGATGCA 2333

RESULT 7

ABK12811
ID ABK12811 standard; DNA; 30676 BP.

XX ABK12811;

XX 18-JUN-2002 (first entry)

XX Human tumour suppressor CAR-1, BAC clone RP11-131M11.

XX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
XX gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
XX colon cancer; stomach cancer; breast cancer; endometrial cancer;
XX prostate cancer; testicular cancer; ovarian cancer; skin cancer;
XX head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
XX bacteriella artificial chromosome; chromosome lp31-lp36.

XX Homo sapiens.

XX WO200212285-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US025269.

XX 10-AUG-2000; 2000US-0225033P.

XX 23-AUG-2000; 2000US-0227560P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Killary A, Chandler D, Lott S;

XX WPI; 2002-269088/31.

XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
XX diagnosing cancer, for altering the phenotype of a tumor cell, for
XX treating cancers or as a diagnostic or prognostic indicator of cancer.

XX Disclosure; Page 176-185; 185pp; English.

XX The invention relates to an isolated polynucleotide encoding a
XX polypeptide being tumor suppressor, CAR-1. Also included are fragments
XX of the polynucleotide from 15-5000 nucleotides, fragments of the protein
XX from 10-50 amino acids, an expression cassette comprising the
XX polynucleotide under the control of a promoter operable in eukaryotic
XX cells, a method for suppressing growth of a cancer cells by contacting
XX the cells with the expression cassette, an anti-CAR-1 monoclonal or
XX comprising the expression cassette, a hybridoma cell that produces the monoclonal
XX antibody, a method of diagnosing a cancer by assessing the expression of
XX CAR-1 tumor suppressor in the cells of a tissue sample from a subject,
XX methods for altering the phenotype of a tumor cell, methods for treating
XX a subject with cancer by administering the tumor suppressor CAR-1 and a
XX promoter active in eukaryotic cells, where the promoter is operably
XX linked to the region encoding the tumor suppressor, a non-human
XX transgenic eukaryote lacking a functional CAR-1 gene, a non-human
XX transgenic eukaryote that over-expresses CAR-1 as compared to a similar
XX non-transgenic eukaryote, a method of screening a candidate substance for
XX anti-tumor activity by contacting a cell lacking functional CAR-1
XX polypeptide, with a candidate substance and determining the effect of the
XX candidate substance on the cell, an anti-tumor composition produced by
XX contacting a cell lacking functional CAR-1 polypeptide, with a candidate
XX substance, determining the effect of the candidate substance on the cell,
XX identifying a candidate inhibitor substance, and making a composition and
XX an isolated and purified nucleic acid that hybridizes, under high
XX stringency conditions, to a DNA segment comprising about 15-3826 bases of
XX the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
XX altering the phenotype of a tumor cell, for treating cancers (e.g.,
XX cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
XX intestine, blood cells, colon, stomach, breast, endometrium, prostate,

CC	testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC	other tissues), and as a diagnostic or prognostic indicator of cancer.
CC	CAR-1 may also be used in screening compounds for activity in either
CC	stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC	effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC	chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC	artificial chromosome) containing part of the CAR-1 gene
XX	
SQ	Sequence 30676 BP; 7591 A; 7621 C; 7888 G; 6944 T; 0 U; 632 Other;
	Query Match 53.2%; Score 2037; DB 6; Length 30676;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 2327; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY	1478 CAGTCCAGCGCCCTAAACCTGGAGCCCGGACACAGCCCAACAGCGCTGATCCTGTCGG 1537
DB	23420 CAGTCCAGCGCCCTAAACCTGGAGCCCGGACACAGCCCAACAGCGCTGATCCTGTCGG 23479
QY	1538 ACGACTGCACCATTTGTGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 1597
DB	23480 ACGACTGCACCATTTGTGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAA 1597
QY	1598 AGCGCTTCGATGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1657
DB	23540 AGCGCTTCGATGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1657
QY	1658 ACTGGAGGTGGTGGTGGCGAGAGAGCCAGTGGGTGATCGGGTGGCACACGAGCGC 1717
DB	23600 ACTGGAGGTGGTGGTGGCGAGAGAGCCAGTGGGTGATCGGGTGGCACACGAGCGC 1717
QY	1718 CAAGCCCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGTGATGC 1777
DB	23660 CAAGCCCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCGTGATGC 1777
QY	1778 ACGATGCAACACCTAGTACAGCGCTGACGAGCCCTGACGCGGCTTCTACTGATCGTGATGC 1837
DB	23719 ACGATGCAACACCTAGTACAGCGCTGACGAGCCCTGACGCGGCTTCTACTGATCGTGATGC 1837
QY	1838 AGCTTGACAGGTGGGTGCTTCTGACTATGACCAAGGCTTCTCATCTTCTACCAATG 1897
DB	23779 AGCTTGACAGGTGGGTGCTTCTGACTATGACCAAGGCTTCTCATCTTCTACCAATG 1897
QY	1898 CTGATGACATGCTCTGCTCTACACCTTCGCGAGAGTTCCCTGGCAAGCTCTGCTCTT 1957
DB	23839 CTGATGACATGCTCTGCTCTACACCTTCGCGAGAGTTCCCTGGCAAGCTCTGCTCTT 1957
QY	1958 ACTTCAGCCCTGCGCAGAGCAGCCAAATGCGAAGACGTTGCGCGCTGCGGATCAACA 2017
DB	23899 ACTTCAGCCCTGCGCAGAGCAGCCAAATGCGAAGACGTTGCGCGCTGCGGATCAACA 2017
QY	2018 CCGTCCGCACTAGTCCAGGCAAGAGAGACCAACCTCCTGGGACCACTGCGCACTGC 2077
DB	23959 CCGTCCGCACTAGTCCAGGCAAGAGAGACCAACCTCCTGGGACCACTGCGCACTGC 2077
QY	2078 AAGAGCCCTGCGCAGAGTACAGACCTGAGCTCCAGCCCACTGCGGCACTGCGGAC 2137
DB	24019 AAGAGCCCTGCGCAGAGTACAGACCTGAGCTCCAGCCCACTGCGGCACTGCGGAC 2137
QY	2138 CTGAGGCCAGTTGTTTACCCCTCCAGCTCCAGTCTGTAATAATGGAGTTGCAATCCCTAC 2197
DB	24078 CTGAGGCCAGTTGTTTACCCCTCCAGCTCCAGTCTGTAATAATGGAGTTGCAATCCCTAC 2197
QY	2198 TTTCCTAACTCTTCCAGCATGATGTTCTGATCTGATCTGATCTGATAGGATACAGCT 2257
DB	24138 TTTCCTAACTCTTCCAGCATGATGTTCTGATCTGATCTGATAGGATACAGCT 2257
QY	2258 TTGATCCAGGATGACATGCTTCTCTAGGGCAACCCCTGCGGCAACCCCTCATCCCC 2317
DB	24198 TTGATCCAGGATGACATGCTTCTCTAGGGCAACCCCTGCGGCAACCCCTCATCCCC 2317
QY	2318 ATCTTCTCAGGGGCGAGGAGCTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 2377
DB	24258 ATCTTCTCAGGGGCGAGGAGCTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 2377
QY	24258 ATCTTCTCAGGGGCGAGGAGCTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCA 24317
DB	

QY	2378 GGAAGTGTGAGAGCATGGCCAGTAGTTGGCAGCCGAAAGACACACAGCACCTCTTATG 2437
DB	24318 GGAAGTGTGAGAGCATGGCCAGTAGTTGGCAGCCGAAAGACACACAGCACCTCTTATG 24377
QY	2438 TCCCATGGCTTAAGCTTACCCCTGACCAAGTAGTGTGGGCCATTTACCTTGAACCC 2497
DB	24378 TCCCATGGCTTAAGCTTACCCCTGACCAAGTAGTGTGGGCCATTTACCTTGAACCC 2497
QY	2498 AGTCCACAGTGTGTCACAGTAGTACCTGCTCCTAGGTTGCTGAGAGCAACCTCTCT 2557
DB	24438 AGTCCACAGTGTGTCACAGTAGTACCTGCTCCTAGGTTGCTGAGAGCAACCTCTCT 24497
QY	2558 GCCACCCCAACACCAAGAACTATATGTTTCTTCTCCCACTGATCTGCTGGTCAGTG 2617
DB	24498 GCCACCCCAACACCAAGAACTATATGTTTCTTCTCCCACTGATCTGCTGGTCAGTG 24557
QY	2618 ATGATGCTGTGGCTGTGGAGGACCTGTGTGTAGTGCACACATTTATGTATGTGC 2677
DB	24558 ATGATGCTGTGGCTGTGGAGGACCTGTGTGTAGTGCACACATTTATGTATGTGC 24617
QY	2678 CACCACCTTCTGCTCCACAGGCCGAGGACAGGGTGGGGTATACCCAAAGCTGATGCAG 2737
DB	24618 CACCACCTTCTGCTCCACAGGCCGAGGACAGGGTGGGGTATACCCAAAGCTGATGCAG 24677
QY	2738 AGCCCATTTAGCTTAAAGCAACTGSCAGGCAAGCCCTCCCTGGATGATCGAGTCCCCAGT 2797
DB	24678 AGCCCATTTAGCTTAAAGCAACTGSCAGGCAAGCCCTCCCTGGATGATCGAGTCCCCAGT 24737
QY	2798 AGCTCTCAAGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGTTG 2857
DB	24738 AGCTCTCAAGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGTTG 24797
QY	2858 CAGGAGCTTCCAGAGCAGTTGTTGTAATTTAGGACCCCAAGCACTGGAGGGGCTGTGG 2917
DB	24798 CAGGAGCTTCCAGAGCAGTTGTTGTAATTTAGGACCCCAAGCACTGGAGGGGCTGTGG 24857
QY	2918 CTAGACCCCTTGTGACATTTGGCATCTATCTCAGTTAGGATCTCTGCTGCAAGAACAGA 2977
DB	24858 CTAGACCCCTTGTGACATTTGGCATCTATCTCAGTTAGGATCTCTGCTGCAAGAACAGA 24917
QY	2978 GCCACTGTGAGCTGTTTAAATTTAGACAGGATTTACTCTGGGCCCTGTGTGGCTTGC 3037
DB	24918 GCCACTGTGAGCTGTTTAAATTTAGACAGGATTTACTCTGGGCCCTGTGTGGCTTGC 24977
QY	3038 AATTGTTGGAAGAGCTGGAAGACAGACTCTGCTGAATTTCCAGGAACCTCCAGCCG 3097
DB	24978 AATTGTTGGAAGAGCTGGAAGACAGACTCTGCTGAATTTCCAGGAACCTCCAGCCG 25037
QY	3098 ATTTCATGCTGTGTTGTGACCAAGAAAGCTGCCCACTCTGCAAGAACCACTATGCCA 3157
DB	25038 ATTTCATGCTGTGTTGTGACCAAGAAAGCTGCCCACTCTGCAAGAACCACTATGCCA 25097
QY	3158 GAAAGCTGTGACTGACAGACTAGGCTCCCTCTGCAACCGTCCGTGCGCAACCAATAGATG 3217
DB	25098 GAAAGCTGTGACTGACAGACTAGGCTCCCTCTGCAACCGTCCGTGCGCAACCAATAGATG 25157
QY	3218 TCCCTGAGGCTTCCCTCTCCCACTTCACTCAGTTTCCCAAAATCTAAATTTTACAGAGA 3277
DB	25158 TCCCTGAGGCTTCCCTCTCCCACTTCACTCAGTTTCCCAAAATCTAAATTTTACAGAGA 25217
QY	3278 TTCTGTTTGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAT 3337
DB	25218 TTCTGTTTGGGGAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAT 25277
QY	3338 GTCAATTTCCCTAGAGGAGTGTGGTGGGTGGAGCAAGCCCACTGCTGCTTTTCTGCC 3397
DB	25278 GTCAATTTCCCTAGAGGAGTGTGGTGGGTGGAGCAAGCCCACTGCTGCTTTTCTGCC 25337
QY	3398 ACAGCATCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTCTCTGC 3457
DB	25338 ACAGCATCAATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTGTCTCTGC 25397


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Db 967 CACGAGCAGCATCAGGTCACCGGCTACGACGACGCTTCGACGAGCTGCAGAGGAGCTG 1026
QY 1021 AAGGACCAACTTCAGGCGCTTCAAGACGCGAGCGGGAACACACGAGCGCTGCAGCTG 1080
Db 1027 AAGGACCAACTTCAGGCGCTTCAAGACGCGAGCGGGAACACACGAGCGCTGCAGCTG 1086
QY 1081 CTCAGCGACAACTCGCGGAGACCAAGTCTTCCACAGAGGCTCGGACCACTATCGG 1140
Db 1087 CTCAGCGACAACTCGCGGAGACCAAGTCTTCCACAGAGGCTCGGACCACTATCGG 1146
QY 1141 GAGGCTTCGAGCGCTGCACCGGCTGCTGTGTAAGCGCCAGAGGCCATGCTAGAGAG 1200
Db 1147 GAGGCTTCGAGCGGCTGCACCGGCTGCTGTGTAAGCGCCAGAGGCCATGCTAGAGAG 1206
QY 1201 CTGAGGCGGACACGCGCGCACGCTGACCGCATCGAGCGAGAAAGTCCAGGCTACAGC 1260
Db 1207 CTGAGGCGGACACGCGCGCACGCTGACCGCATCGAGCGAGAAAGTCCAGGCTACAGC 1266
QY 1261 CAGCAGCTGCGCAAGGTCAGGAGGAGCGCCAGATCTCTGCGAGGCGGCTGCTGAAACC 1320
Db 1267 CAGCAGCTGCGCAAGGTCAGGAGGAGCGCCAGATCTCTGCGAGGCGGCTGCTGAAACC 1326
QY 1321 GACCGGCACACTTCCTGCTGGGTGGGCTCACTGTCCGAGCGGCTCAAGGGAAAATC 1380
Db 1327 GACCGGCACACTTCCTGCTGGGTGGGCTCACTGTCCGAGCGGCTCAAGGGAAAATC 1386
QY 1381 CATGAGACCAACTTCACATATGAAGACTTCCGACCTCCAGTACACAGGCGGCTGCGAG 1440
Db 1387 CATGAGACCAACTTCACATATGAAGACTTCCGACCTCCAGTACACAGGCGGCTGCGAG 1446
QY 1441 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCGGCTAACCTG 1500
Db 1447 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCGGCTAACCTG 1506
QY 1501 GACCGGGACAGCCACAGCGGCTGATCTGTGCGAGCACTSCACCATTTGGCTTAC 1560
Db 1507 GACCGGGACAGCCACAGCGGCTGATCTGTGCGAGCACTSCACCATTTGGCTTAC 1566
QY 1561 GGCAACTTGCAACACACAGCCACTGCAGGACTCGCCAAAGCGCTCGATGTGAGGTGTCG 1620
Db 1567 GGCAACTTGCAACACACAGCCACTGCAGGACTCGCCAAAGCGCTTCGATGTGAGGTGTCG 1626
QY 1621 GTGCTGGTTCAGAGCTTCAGTGTGCGTCCACTACTGGAGGTGGTGGTGGCGGAG 1680
Db 1627 GTGCTGGTTCAGAGCTTCAGTGTGCGTCCACTACTGGAGGTGGTGGTGGCGGAG 1686
QY 1681 AAGACCCAGTGGGTGATCGGCTGGCACAGAGCGCGAAGCGCGAAGGCGAGCTCCAG 1740
Db 1687 AAGACCCAGTGGGTGATCGGCTGGCACAGAGCGCGAAGCGCGAAGGCGAGCTCCAG 1746
QY 1741 ATCCAG 1746
Db 1747 ATCCAG 1752
```

RESULT 9

```
ADC37454
ID ADC37454 standard; DNA; 2207 BP.
XX
AC ADC37454;
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 287.
XX
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Antinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
XX
OS Homo sapiens.
```

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XX
PN WO2003048202-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002WO-JP012644.
XX
PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
PA (ASAH ) ASAMI KASEI KK.
XX
PI Matsuda A, Muramatsu S;
XX
DR WPI; 2003-505282/47.
DR P-PSDB; ADC37455.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
PS Claim 4; SEQ ID NO 287; 938pp; English.
XX
CC The present invention relates to novel proteins and their coding
CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.
XX
SQ Sequence 2207 BP; 414 A; 784 C; 618 G; 391 T; 0 U; 0 Other;

Query Match 32.1%; Score 1230; DB 9; Length 2207;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 466 CCCTTCTCCGGTAGCTACCCCTGCTGCGGCGCTTGTCCCGCGCCAGCCCTCG 525
Db 433 CCCTTCTCCGGTAGCTACCCCTGCTGCGGCGCTTGTCCCGCGCCAGCCCTCG 492
QY 526 GTGCTGCTCCGACAGCGCGGCTCTCTCAGCGCGCCCTGCTGCGGCGCCCTC 585
Db 493 GTGCTGCTCCGACAGCGCGGCTCTCTCAGCGCGCCCTGCTGCGGCGCCCTC 552
QY 586 TCTGCTGCGGCGCGGCTGCGGCTCAGCTCAGGACGAGTGTGCTCCATCTGC 645
Db 553 TCTGCTGCGGCGCGGCTGCGGCTCAGCTCAGGACGAGTGTGCTCCATCTGC 612
QY 646 CTGAGCATCTACAGGACCGGCTGAGCGCTGCGGCTGCGGCGCGGCGGCGGCTG 705
Db 613 CTGAGCATCTACAGGACCGGCTGAGCGCTGCGGCTGCGGCGCGGCGGCTG 672
QY 706 ATCAGGAGCACTGGGTGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 765
Db 673 ATCAGGAGCACTGGGTGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732
QY 766 GCGCAGTTCGCGGAGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 825
Db 733 GCGCAGTTCGCGGAGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 792
QY 826 TACAGCTCTTCCCGCTGAGCGCATCTCAACGCGCGCGCGCGCGCGCGCGCGG 885
Db 793 TACAGCTCTTCCCGCTGAGCGCATCTCAACGCGCGCGCGCGCGCGCGCGCGG 852
QY 886 GCGCAGCAAGGTCAAGCTTCTGCGCTCAGGACCGCGGCGGCTTCTGCTTCTTTCG 945
Db 853 GCGCAGCAAGGTCAAGCTTCTGCGCTCAGGACCGCGGCGGCTTCTGCTTCTTTCG 912
QY 946 GACGAGCTGCACTGCAGGACGAGCATCAGTCCAGGCGATCGAGCGCTTCGACGAG 1005
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Db	1334	AAAGATCCAGGCAACCCCTCTTT	CAGCCAGGSCCTCTGTGACCTGCTAGGGTGCAGAGGCTT	1393
QY	2868	CCAGAAGCAGTGTGTGTAATTTAG	AGACCCCAAGCACT- GGGAGGGCTGTGTGGCTAGACCCC	2926
Db	1394	CCAGAAGCAGTGTGTGTAATTTAG	AGACCCCAAGCACTGGGGAGGGGCTGTGTGGCTAAACCCC	1453
QY	2927	TTGTCCAGACTTGGCATCTATCTC	AGTTAGGATCTGTGTCAGAAAAACAAGAGCCACTTGT	2986
Db	1454	TTGTCCAGACTTGGCATCTATCTC	AGTTAGGATCTGTGTCAGAAAAACAAGAGCCACTTGT	1513
QY	2987	AGCTGGTTTAATTTAGACAAGGAT	TTTACTATCTGTGGCCCTGTGTGGCTTGCRAAATTTGTGG	3046
Db	1514	AGCTGGTTTAATTTAGACAAGGAT	TTTACTATCTGTGGCCCTGTGTGGCTTGCRAAATTTGTGG	1573
QY	3047	AAGAGCTGGAGAAGCAGACTCTG	CTGTAATTTCCAGGACTCCACGCGCAGATTCATCAT	3106
Db	1574	AAGAGCTGGAGAAGCAGACTCTG	CTGTAATTTCCAGGAACTCCACGCGCAGATTCATCAT	1633
QY	3107	GTCTGTTGTGACCAGGAAGCTGC	CCCATCTGTCAGGAAGCCACTATGTCAGAAAGCTGC	3166
Db	1634	GTCTGTTGTGACCAGGAAGCTGC	CCCATCTGTCAGGAAGCCACTATGTCAGAAAGCTGC	1693
QY	3167	TGACTGCGAGACTAGGCTCCCTCT	GCCACAGGTCGTCGACCAATAGATGTCTGTGAGGC	3226
Db	1694	TGACTGCGAGACTAGGCTCCCTCT	GCCACAGGTCGTCGACCAATAGATGTCTGTGAGGC	1753
QY	3227	CTGCCCCCTCTCCCACTTCACTC	AGTTCCTCCAAATCTAAATTTTATACAGAGATTCGTGTTG	3286
Db	1754	CTGCCCCCTCTCCCACTTCACTC	AGTTCCTCCAAATCTAAATTTTATACAGAGATTCGTGTTG	1813
QY	3287	GGGGAACTTTAAGTCAGATCCAG	AACCTTGGCTGCAAGGGAGTCTGGGAAATGTCAATTTCC	3346
Db	1814	GGGGAACTTTAAGTCAGATCCAG	AACCTTGGCTGCAAGGGAGTCTGGGAAATGTCAATTTCC	1873
QY	3347	CTAGAAGGAAGTTAGGTTGGGTG	GAGCAAGCCCACTCTGGCTTTTCTGCGCACAGATCC	3406
Db	1874	CTAGAAGGAAGTTAGGTTGGGTG	GAGCAAGCCCACTCTGGCTTTTCTGCGCACAGATCC	1933
QY	3407	AATCGTGAAGAACTCGGAGAGGG	TGGAGTCCACATCTAGGGTTGTCTGCGCCCTTTGGCT	3466
Db	1934	AATCGTGAAGAACTCGGAGAGGG	TGGAGTCCACATCTAGGGTTGTCTGCGCCCTTTGGCT	1993
QY	3467	CTATCCCTGCCAGAGTGGGAATG	GAGAGTGGGCTGCAAGCTGAGCCTAAATGTCT	3526
Db	1994	CTATCCCTGCCAGAGTGGGAATG	GAGAGTGGGCTGCAAGCTGAGCCTAAATGTCT	2053
QY	3527	CCCCGGCCTTGAATTTTCTTTCT	TAGTCTTCTAGTCTGGGCTTAGATCTGCACTTTGGGCTCTCTGA	3586
Db	2054	CCCCGGCCTTGAATTTTCTTTCT	TAGTCTTCTAGTCTGGGCTTAGAATCTGCACTTTGGGCTCTCTGA	2113
QY	3587	CACAAACACCATTCCAAAGTAG	CCGGAAGACTAAACACAGGGGTTCTTAAATGGCT	3646
Db	2114	CACAAACACCATTCCAAAGTAG	CCGGAAGACTAAACACAGGGGTTCTTAAATGGCT	2173
QY	3647	GCCCCCGCACCCGGGCTCCCTCT	TGGGCAAAAGGATTCGACGCCCTACCCAAACCCCTTC	3706
Db	2174	GCCCCCGCACCCGGGCTCCCTCT	TGGGCAAAAGGATTCGACGCCCTACCCAAACCCCTTC	2233
QY	3707	AATCTACAGAACTGGGCCACCCC	CAGCAGTATTTTATTTAAATAGTTGCCCATTTTATG	3766
Db	2234	AATCTACAGAACTGGGCCACCCC	CAGCAGTATTTTATTTAAATAGTTGCCCATTTTATG	2293
QY	3767	AGTTATGATCAATTTGTATTAAT	TAAATTAAGATTACAGATGCA	3807
Db	2294	AGTTATGATCAATTTGTATTAAT	TAAATTAAGATTACAGATGCA	2334

18-JUN-2002 (first entry)
Human tumour suppressor CAR-1, BAC clone 392H05 3' sequence.

Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
colon cancer; stomach cancer; breast cancer; endometrial cancer;
prostate cancer; testicular cancer; ovarian cancer; skin cancer;
head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
bacteria artificial chromosome; chromosome lp31-1p36.

Homo sapiens.

WO200212285-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US025269.

10-AUG-2000; 2000US-0225033P.
23-AUG-2000; 2000US-0227560P.

(TEXA) UNIV TEXAS SYSTEM.

Killary A, Chandler D, Lott S;
WPI; 2002-269088/31.

The invention relates to an isolated polynucleotide encoding a polypeptide being tumour suppressor, CAR-1. Also included are fragments of the polynucleotide from 15-5000 nucleotides, fragments of the protein from 10-50 amino acids, an expression cassette comprising the polynucleotide under the control of a promoter operable in eukaryotic cells, a method for suppressing growth of a cancer cells by contacting the cells with the expression cassette (i.e. gene therapy), a cell comprising the expression cassette, an anti-CAR-1 monoclonal or polyclonal antibody, a hybridoma cell that produces the monoclonal antibody, a method of diagnosing a cancer by assessing the expression of CAR-1 tumour suppressor in the cells of a tissue sample from a subject, methods for altering the phenotype of a tumour cell, methods for treating a subject with cancer by administering the tumour suppressor CAR-1, or by administering a nucleic acid encoding the tumour suppressor CAR-1 and a promoter active in eukaryotic cells, where the promoter is operably linked to the region encoding the tumour suppressor, a non-human transgenic eukaryote lacking a functional CAR-1 gene, a non-human transgenic eukaryote that over-expresses CAR-1 as compared to a similar non-transgenic eukaryote, a method of screening a candidate substance for anti-tumour activity by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance and determining the effect of the candidate substance on the cell, an anti-tumour composition produced by contacting a cell lacking functional CAR-1 polypeptide, with a candidate substance, determining the effect of the candidate substance on the cell, identifying a candidate inhibitor substance, and making a composition and an isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15-3826 bases of the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for altering the phenotype of a tumour cell, for treating cancers (e.g. cancer of the brain, lung, liver, kidney, lymph node, pancreas, small intestine, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or other tissues), and as a diagnostic or prognostic indicator of cancer. CAR-1 may also be used in screening compounds for activity in either stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the effect of mutant CAR-1 molecule. The gene for CAR-1 is located on chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial artificial chromosome) containing part of the CAR-1 gene.

RESULT 12
ABK12808
ID ABK1
XX
AC ABK1

XX	SQ	Sequence 30625 BP; 8084 A; 7712 C; 7487 G; 7314 T; 0 U; 28 Other;	
		Query Match 24.3%; Score 928; DB 6; Length 30625;	
		Best Local Similarity 99.2%; Pred. No. 0;	
		Matches 1648; Conservative 0; Mismatches 12; Indels 1; Gaps 1;	
QY	2148	TTGTTTACCCCTCCAGCCTCCAGTCTGTPAAATGAGGTTGATTCCTTCTTAACT 2207	
DB	22623	TTGTTTACCCCTCCAGCCTCCAGTCTGTPAAATGAGGTTGATTCCTTCTTAACT 22682	
QY	2208	CTCTTCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTTGATCCAAG 2267	
DB	22683	CTCTTCAGCATCGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTTGATCCAAG 22742	
QY	2268	GATGTGACATGGCTTCTCTCCAGGGCAACCCCTCCCAACCCCTCATCCCATCTTCTCAG 2327	
DB	22743	GATGTGACATGGCTTCTCTCCAGGGCAACCCCTCCCAACCCCTCATCCCATCTTCTCAG 22802	
QY	2328	GGGAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTC 2387	
DB	22803	GGGAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTC 22862	
QY	2388	GAGCATGGCAGTAGTTGGCAGCCCGAAGACACACAGCACCCCTTATGTGCCATGGCC 2447	
DB	22863	GAGCATGGCAGTAGTTGGCAGCCCGAAGACACACAGCACCCCTTATGTGCCATGGCC 22922	
QY	2448	TAAGACTTACCCCTGACCAAGCTAGTGTAGTGGCCATTTTACCCCTTGACCCCACTCCACAGT 2507	
DB	22923	TAAGACTTACCCCTGACCAAGCTAGTGTAGTGGCCATTTTACCCCTTGACCCCACTCCACAGT 22982	
QY	2508	GGTCACAGGTAGTACCTGGTCTAGGGTTGCTGAGAGCCAACTCTCTCTGCCACCCCA 2567	
DB	22983	GGTCACAGGTAGTACCTGGTCTAGGGTTGCTGAGAGCCAACTCTCTCTGCCACCCCA 23042	
QY	2568	CACCAAGACTATATGGTTCTTACTTCTCCCACTGATCTGTGTGTCAGTGATGCTGT 2627	
DB	23043	CACCAAGAAATATATGGTTCTTACTTCTCCCACTGATCTGTGTGTCAGTGATGCTGT 23102	
QY	2628	GGCTGTGGAAGGCACCTGGTGTGAGTCCACACATTATAGTCAATGTGCCACCACTTC 2687	
DB	23103	GGCTGTGGAAGGCACCTGGTGTGAGTCCACACATTATAGTCAATGTGCCACCACTTC 23162	
QY	2688	CTGCCACAGCGCGAGGACAGGGTGAGGGTATACCAAGCTGATGACAGCCCATTTAG 2747	
DB	23163	CTGCCACAGCGCGAGGACAGGGTGAGGGTATACCAAGCTGATGACAGCCCATTTAG 23222	
QY	2748	CCTAAAGCAACTGCGAGGACAGCCCTCCCTGGATGATCAGGTCCCACTGTCTGAACT 2807	
DB	23223	CCTAAAGCAACTGCGAGGACAGCCCTCCCTGGATGATCAGGTCCCACTGTCTGAACT 23282	
QY	2808	AAGAGTCCAGCAACCCCTCTCAGCCAGGCCTCTGTGACCTGTAGGGTGACGAGGCTT 2867	
DB	23283	AAGAGTCCAGCAACCCCTCTCAGCCAGGCCTCTGTGACCTGTAGGGTGACGAGGCTT 23342	
QY	2868	CCAGAAGCGATGTTGTAATAGGACCCCAAGCACT-CCGAGGGGCTGTGGCTAGACCCC 2926	
DB	23343	CCAGAAGCGATGTTGTAATAGGACCCCAAGCACT-CCGAGGGGCTGTGGCTTAACCCC 23402	
QY	2927	TTGTGACATTTGCACTCTATCTCAGTGTAGTATCTCTGTCAGAAAAACAAGAGCCATTGT 2986	
DB	23403	TTGTGACATTTGCACTCTATCTCAGTGTAGTATCTCTGTCAGAAAAACAAGAGCCATTGT 23462	
QY	2987	AGCTGGTTTTAAATPAGCAAGGATTTTACTAGTGGCCCTGTGGCTGTGCAAAATTTGTG 3046	
DB	23463	AGCTGGTTTTAAATPAGCAAGGATTTTACTAGTGGCCCTGTGGCTGTGCAAAATTTGTG 23522	
QY	3047	AAGAGCTGGAAGAGCAGACTCTGTAATTTCCAGGAACCTCCAGCGCCAGATTTCATCAT 3106	
DB	23523	AAGAGCTGGAAGAGCAGACTCTGCTGTAATTTCCAGGAACCTCCAGCGCCAGATTTCATCAT 23582	
QY	3107	GTCTGTGTGTGACCAAGAAAGCTGCCCCCATCTCGAAGAGCCCATGTGCCAGAAAGCTGC 3166	

DB	23583	GTCTGTGTGTGACCAAGAAAGCTGCCCCCATCTCGAGAAAGCCACTATGCCAGAAAGCTGC 23642	
QY	3167	TGACTGCAGAACTAGGCTCCCTCTGCCAGGCTCCGTGCCAGCAATAGATGTCTCTGAGGC 3226	
DB	23643	TGACTGCAGAACTAGGCTCCCTCTGCCAGGCTCCGTGCCAGCAATAGATGTCTCTGAGGC 23702	
QY	3227	CTGCCCTCTCTCCACATTTCACTCAGTTTCCAAAATCTAAATTTTACAAGAGATTCTGTTG 3286	
DB	23703	CTGCCCTCTCTCCACATTTCACTCAGTTTCCAAAATCTAAATTTTACAAGAGATTCTGTTG 23762	
QY	3287	GGGAACTTAAGTCAGATCCAGAACCTTGGCTCAAGGGAGCTCGGGAATGTCATTTCC 3346	
DB	23763	GGGAACTTAAGTCAGATCCAGAACCTTGGCTCAAGGGAGCTCGGGAATGTCATTTCC 23822	
QY	3347	CTAGAAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTCGGTCTTCTGCCACAGCATCC 3406	
DB	23823	CTAGAAGGAAGTTAGGCTGGGTGGAGCAAGCCCACTCGGTCTTCTGCCACAGCATCC 23882	
QY	3407	AATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCCCCCTGGCT 3466	
DB	23883	AATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGGTTGTCTGCCCCCTGGCT 23942	
QY	3467	CTATCCCTGCCAGAGGTGGAACTCGGAGGAGTGGGCTGCAAGACTGAGCCTTAATGTCT 3526	
DB	23943	CTATCCCTGCCAGAGGTGGAACTCGGAGGAGTGGGCTGCAAGACTGAGCCTTAATGTCT 24002	
QY	3527	CCCGGGCTTCTGACCTTTCTTTCTAGTCTCGGGGCTAGATTTCTGCACCTTGGGGTCTCTGA 3586	
DB	24003	CCCGGGCTTCTGACCTTTCTTTCTAGTCTCGGGGCTAGATTTCTGCACCTTGGGGTCTCTGA 24062	
QY	3587	CACAACACACCATCCCAAAGTAGCGGAGAGCTAAACACAGGGGTTCTTAAATGGCT 3646	
DB	24063	CACAACACACCATCCCAAAGTAGCGGAGAGCTAAACACAGGGGTTCTTAAATGGCT 24122	
QY	3647	GGCCCGGACCCCGGCTTCCCTTGGGCAAGGAATGTGAGCCCTTACCCCAACCCCTC 3706	
DB	24123	GGCCCGGACCCCGGCTTCCCTTGGGCAAGGAATGTGAGCCCTTACCCCAACCCCTC 24182	
QY	3707	AATACACAGAACTCGGGCCACCCCAAGCAGTATTTTATTTAAATGTTGCCCATTTATG 3766	
DB	24183	AATACACAGAACTCGGGCCACCCCAAGCAGTATTTTATTTAAATGTTGCCCATTTATG 24242	
QY	3767	AGTTATGATCAATTTGTTATTAATTAAGTTTACAGATGTCA 3807	
DB	24243	AGTTATGATCAATTTGTTATTAATTAAGTTTACAGATGTCA 24283	

RESULT 13
ABK12809
ID ABK12809 standard; DNA; 45845 BP.
XX
AC ABK12809;
XX
DT 18-JUN-2002 (first entry)
XX
Human tumour suppressor CAR-1, BAC clone RP11-150F21 5' sequence.
Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
colon cancer; stomach cancer; breast cancer; endometrial cancer;
prostate cancer; testicular cancer; ovarian cancer; skin cancer;
head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
bacteria artificial chromosome; chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX
PN WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PF 10-AUG-2000; 2000US-0225033P.

Db	573	CTTCGATGTGGAGGTGTCGGTGTGGGTCTGAAGCCCTTCAGTAGTGGCTCCACTACTG	514
Qy	1662	GGAGGTGGTGGTGGCGAGAAAGCCACGTGGGTGATCGGGCTGGCACACGAAGCCCAAG	1721
Db	513	GGAGGTGGTGGTGGCGAGAAAGCCACGTGGGTGATCGGGCTGGCACACGAAGCCCAAG	454
Qy	1722	CCGCAAGGGCAGCATCCAGATCCAGGCCAGCCGGGGTCTTACTGTCATCGTGTGACACGA	1781
Db	453	CCGCAAGGGCAGCATCCAGATCCAGGCCAGCCGGGGTCTTACTGTCATCGTGTGACACGA	394
Qy	1782	TGGCAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGGGCTTAAAGTCCGGGACAAAGCT	1841
Db	393	TGGCAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGGGCTTAAAGTCCGGGACAAAGCT	334
Qy	1842	TGACAAAGTGGGTGTCCTCTCGACTATGACCAAGGTTGCTCATCTTCTACAAATGCTGA	1901
Db	333	TGACAAAGTGGGTGTCCTCTCGACTATGACCAAGGTTGCTCATCTTCTACAAATGCTGA	274
Qy	1902	TGACATGTCCTGGCTCTACACCTTCCGCGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTT	1961
Db	273	TGACATGTCCTGGCTCTACACCTTCCGCGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTT	214
Qy	1962	CAGCCCTGGCCAGAGCCACGCCAATGCGAAGACGTTACGCCGTGGGATCAACACCGT	2021
Db	213	CAGCCCTGGCCAGAGCCACGCCAATGCGAAGACGTTACGCCGTGGGATCAACACCGT	154
Qy	2022	CCGCATCTTAGTCCAGGCAGAGGAGACCAACCTCCTGGGACCACTGCCACCTGCGAAGA	2081
Db	153	CCGCATCTTAGTCCAGGCAGAGGAGACCAACCTCCTGGGACCACTGCCACCTGCGAAGA	94
Qy	2082	GCCTGCCACAGGA	2094
Db	93	GCCTGCCACAGGA	81

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2: /cgn2.6/prodata/2/ina/5B COMB.seq.*
3: /cgn2.6/prodata/2/ina/6A COMB.seq.*
4: /cgn2.6/prodata/2/ina/6B COMB.seq.*
5: /cgn2.6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2.6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	25	0.7	469	1	US-08-468-347-23
2	25	0.7	469	1	US-08-226-264-25
3	25	0.7	469	1	US-08-467-389-23
4	25	0.7	469	2	US-08-779-379-23
5	25	0.7	469	2	US-08-469-219-23
6	25	0.7	469	3	US-09-228-152-23
7	25	0.7	729	1	US-08-447-010-1
8	25	0.7	868	3	US-08-889-502-20
9	25	0.7	9844	4	US-09-791-211-10
10	24	0.6	40	3	US-09-306-290-26
11	24	0.6	555	4	US-09-449-285A-15
12	24	0.6	1196	3	US-07-959-509-4
13	24	0.6	1332	3	US-09-333-423-1
14	24	0.6	1392	4	US-08-957-351-1
15	24	0.6	1478	4	US-09-216-393B-7
16	24	0.6	1496	4	US-09-712-529-1
17	24	0.6	1628	2	US-08-883-515-3
18	24	0.6	1705	4	US-09-205-258-216
19	24	0.6	2017	3	US-09-436-983-1
20	24	0.6	2193	4	US-09-427-261-2
21	24	0.6	2193	4	US-09-427-261-3
22	24	0.6	3001	4	US-09-539-333D-222
23	24	0.6	3848	3	US-09-112-096-28
24	24	0.6	3952	2	US-08-381-691-16
25	24	0.6	5668	3	US-09-112-096-14
26	24	0.6	5668	4	US-09-636-215-777
27	24	0.6	5668	4	US-09-685-166A-777

c 28 24 0.6 21234 4 US-09-810-671-3 Sequence 3, Appli
c 29 24 0.6 21234 4 US-10-109-854-3 Sequence 3, Appli
c 30 24 0.6 32042 4 US-09-245-281-44 Sequence 44, Appli
c 31 24 0.6 32042 4 US-09-340-620A-63 Sequence 63, Appli
c 32 24 0.6 50000 4 US-08-146-053-3 Sequence 3, Appli
c 33 24 0.6 786431 4 US-09-751-389-3 Sequence 3, Appli
c 34 23 0.6 40 3 US-09-306-290-15 Sequence 15, Appli
35 23 0.6 67 4 US-09-621-976-10956 Sequence 10956, A
36 23 0.6 97 4 US-09-621-976-9086 Sequence 9086, App
37 23 0.6 307 4 US-09-091-725-28 Sequence 28, Appl
38 23 0.6 350 4 US-09-621-976-15342 Sequence 15342, A
39 23 0.6 433 1 US-07-987-272A-13 Sequence 13, Appl
40 23 0.6 567 1 US-08-661-168-6 Sequence 6, Appli
41 23 0.6 627 3 US-09-385-982-4 Sequence 4, Appli
42 23 0.6 989 2 US-08-874-460-1 Sequence 1, Appli
43 23 0.6 989 4 US-09-272-162-1 Sequence 1, Appli
44 23 0.6 1005 4 US-09-647-224A-5 Sequence 5, Appli
45 23 0.6 1087 4 US-09-396-149-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-468-347-23
; Sequence 23, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-468-347-23

Query Match 0.7%; Score 25; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.37;

us-09-927-091-3.01i15.rni

Mon Aug 2 10:03:35 2004

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 2

US-08-226-264-25
 ; Sequence 25, Application US/08226264
 ; Patent No. 5801017
 ; GENERAL INFORMATION:
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Levanon, Avigdor
 ; APPLICANT: Guy, Rachel
 ; APPLICANT: Goldlust, Arie
 ; APPLICANT: Rigbi, Meir
 ; APPLICANT: Panet, Amos
 ; APPLICANT: Fischer, Meir
 ; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
 ; TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 08-APR-94
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 25:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 469 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-226-264-25

Query Match 0.7%; Score 25; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 3

US-08-467-389-23
 ; Sequence 23, Application US/08467389
 ; Patent No. 5824641
 ; GENERAL INFORMATION:
 ; APPLICANT: Zeelon, Elisha P.

APPLICANT: Werber, Moshe M.
 APPLICANT: Levanon, Avigdor
 TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
 TITLE OF INVENTION: INHIBITORY ACTIVITY
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,389
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/225,442
 FILING DATE: 08-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-977-9550
 TELEFAX: 212-664-0525
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-08-467-389-23

Query Match 0.7%; Score 25; DB 1; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
 Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 4

US-08-779-379-23
 ; Sequence 23, Application US/08779379
 ; Patent No. 5858970
 ; GENERAL INFORMATION:
 ; APPLICANT: Zeelon, Elisha P.
 ; APPLICANT: Werber, Moshe M.
 ; APPLICANT: Levanon, Avigdor
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
 ; TITLE OF INVENTION: INHIBITORY ACTIVITY
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,379
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-779-379-23

Query Match 0.7%; Score 25; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 5
US-08-469-219-23
Sequence 23, Application US/08469219
Patent No. 5863534
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,219
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-469-219-23

Query Match 0.7%; Score 25; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 6
US-09-228-152-23
Sequence 23, Application US/09228152
Patent No. 6211341
GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 469
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
OTHER INFORMATION: of clone PSP65-Xa1-4.
US-09-228-152-23

Query Match 0.7%; Score 25; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. NO. 0.37;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
Db 445 ATGTCAAAAAAAAAAAAAAAAAAAAA 469

RESULT 7
US-08-447-010-1
Sequence 1, Application US/08447010
Patent No. 5770718
GENERAL INFORMATION:
APPLICANT: MOFFATT, BARBARA
TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/447,010
FILING DATE: 22-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/230,695
FILING DATE: 21-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,132
FILING DATE: 26-MAY-1992
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1811-183 MIS:VG
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(18..569)
US-08-447-010-1

Query Match 0.7%; Score 25; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA 3826
DB 705 ATGTCACAAAAA 729

RESULT 8
US-08-889-502-20
; Sequence 20, Application US/0889502
; Patent No. 6066726
; GENERAL INFORMATION:
; APPLICANT: Farb, David H
; APPLICANT: Russek, Shelley J
; TITLE OF INVENTION: GENE THERAPY VECTOR WITH TISSUE
; TITLE OF INVENTION: SPECIFICITY
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,502
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: 0146-2008
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 868 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-889-502-20

Query Match 0.7%; Score 25; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA 3826
DB 440 ATGTCACAAAAA 464

RESULT 9
US-09-791-211-10/c
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65469
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65470
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 87130
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 89049
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-10

Query Match 0.7%; Score 25; DB 4; Length 98844;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA 3826
DB 95450 ATGTCACAAAAA 95426

RESULT 10
US-09-306-290-26/c

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; Sequence 26, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; APPLICANT: Mukhopadhyay, Sunil
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; TITLE OF INVENTION: (SPADT) USING MULTIARRAYS
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer p41
; OTHER INFORMATION: FH440
US-09-306-290-26

Query Match          0.6%; Score 24; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 24 TGTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
US-09-449-285A-15/c
; Sequence 15, Application US/09449285A
; Patent No. 6313280
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-4232US
; CURRENT APPLICATION NUMBER: US/09/449,285A
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; PRIOR FILING DATE: 1997-06-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 15
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (382)..(555)
; OTHER INFORMATION: n can be any nucleotide
US-09-449-285A-15

Query Match          0.6%; Score 24; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 24 TGTCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 12
US-07-959-509-4
; Sequence 4, Application US/07959509
; Patent No. 6001560
; GENERAL INFORMATION:
; APPLICANT: Ionial, Herinder
; APPLICANT: Narula, Satwant
; APPLICANT: Zavodny, Paul
```

```
; TITLE OF INVENTION: Human Gamma Interferon Antagonist/Agonist Screen
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 4.00B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,509
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/616,621
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 6001560man C.
; REGISTRATION NUMBER: 31,608
; REFERENCE/DOCKET NUMBER: JB0166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 822 7375
; TELEFAX: 201 822 7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-959-509-4

Query Match          0.6%; Score 24; DB 3; Length 1196;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 327 TGTCAAAAAAAAAAAAAAAAAAAAAA 350

RESULT 13
US-09-333-423-1
; Sequence 1, Application US/09333423
; Patent No. 6265636
; GENERAL INFORMATION:
; APPLICANT: Randall, Douglas
; APPLICANT: Thelen, Jay
; APPLICANT: Miernyk, Jan
; APPLICANT: Muszynski, Michael
; APPLICANT: Sewalt, Vincent
; TITLE OF INVENTION: Pyruvate Dehydrogenase Kinase
; TITLE OF INVENTION: Polynucleotides, Polypeptides and Uses Thereof
; FILE REFERENCE: 0818
; CURRENT APPLICATION NUMBER: US/09/333,423
; CURRENT FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,998
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)...(1095)
US-09-333-423-1
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 05:58:02 ; Search time 1597 Seconds
(without alignments)
11746.659 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 15
Total number of hits satisfying chosen parameters: 314177

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2037	53.2	30676	9	US-09-927-091-8
4	928	24.3	30625	9	US-09-927-091-5
5	788	20.6	45845	9	US-09-927-091-6
C 6	575	15.0	610	13	US-10-027-632-100265
C 7	575	15.0	610	16	US-10-027-632-100265
C 8	493	12.9	4731	9	US-09-864-761-7231
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C 10	149	3.9	49744	9	US-09-927-091-4
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C 14	27	0.7	248436	13	US-10-087-192-2014

15	26	0.7	273	12	US-09-969-034-4195	Sequence 4195, Ap
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C 17	26	0.7	411	9	US-09-960-352-13315	Sequence 13315, A
18	26	0.7	4702	16	US-10-295-027-141	Sequence 141, App
19	26	0.7	4702	16	US-10-295-027-1164	Sequence 1164, Ap
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43	25	0.7	430	10	US-09-918-995-7699	Sequence 7699, Ap
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C 45	25	0.7	467	15	US-10-198-846-1221	Sequence 1221, Ap

ALIGNMENTS

RESULT 1
US-09-927-091-3
; Sequence 3, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3826
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-3

Query Match	100.0%;	Score	3826;	DB	9;	Length	3826;
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		Gaps	0;				
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US-09-927-091-8

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; Sequence 01, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30676
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (6671)..(30676)
; OTHER INFORMATION: n = A or C or G or T/U
; US-927-091-8

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Query Match

Query Match	Score 2037; DB 9; Length 30676;
Best Local Similarity	53.28;
Best Local Similarity	99.98;
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Best local similarity 99.9%; Pred. No. 0;
Matches 2327: Conservative 0: Mismatches

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Db	25458	TAAATGTCCTCCCGGCTTGACATTTCTTTCTAGTCTCTGGGCTTAGATTCGCACTTGG	25517
QY	3578	GCTCTCTGACACACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTT	3637
Db	25518	GCTCTCTGACACACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTT	25577
QY	3638	AAAAATGGCTGCCCGGCCACCCGGGCTTCCCTTGGGCAAAAGGAAATGTCAGCCCTACCC	3697
Db	25578	AAAAATGGCTGCCCGGCCACCCGGGCTTCCCTTGGGCAAAAGGAAATGTCAGCCCTACCC	25637
QY	3698	CAACCCCTTCAACTACCAAGATCTGGGCCACCCAGAGAGTATTTTATTTAAAATGTTGCC	3757
Db	25638	CAACCCCTTCAACTACCAAGATCTGGGCCACCCAGAGAGTATTTTATTTAAAATGTTGCC	25697
QY	3758	CATTTATGAGTTATGATCAATTTGATTAATAATTAAGTTACAGATGTCA	3807
Db	25698	CATTTATGAGTTATGATCAATTTGATTAATAATTAAGTTACAGATGTCA	25747
RESULT 4			
US-09-927-091-5			
; Sequence 5, Application US/09927091			
; Patent No. US20020119541A1			
; GENERAL INFORMATION:			
; APPLICANT: KILLARY, ANN			
; APPLICANT: CHANDLER, DAWN			
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1			
; FILE REFERENCE: UTSC:651US			
; CURRENT APPLICATION NUMBER: US/09/927,091			
; CURRENT FILING DATE: 2001-08-09			
; PRIOR APPLICATION NUMBER: 60/227,560			
; PRIOR FILING DATE: 2000-08-23			
; PRIOR APPLICATION NUMBER: 60/225,033			
; PRIOR FILING DATE: 2000-08-10			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 5			
; LENGTH: 30625			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: modified base			
; LOCATION: (4754)..(30625)			
; OTHER INFORMATION: n = A or C or G or T/U			
US-09-927-091-5			
Query Match			
24.3%; Score 928; DB 9; Length 30625;			

Query Match 24.3%; Score 928; DB 9; Length 30625;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1648; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 3227 CTGCCCTCTCCACTTCACTCAGTTCCTCCAAATCTAAATTTTACAGAGATTCGTGTTG 3286
Db |||||
QY 23703 CTGCCCTCTCCACTTCACTCAGTTCCTCCAAATCTAAATTTTACAGAGATTCGTGTTG 23762
Db |||||
QY 3287 GGGAACTTAAGTCAGATCCAGACCTTGGTGCAGGAGTCTGGGAAATGTCAATTTCC 3346
Db |||||
QY 23763 GGGAACTTAAGTCAGATCCAGAACTTGGTGCAGGAGTCTGGGAAATGTCAATTTCC 23822
Db |||||
QY 3347 CTAGAAGAACTTAAGTGGGTGGAGCAAGCCACCTGCGTTTCTGTCACAGATCC 3406
Db |||||
QY 23823 CTAGAAGAACTTAAGTGGGTGGAGCAAGCCACCTGCGTTTCTGTCACAGATCC 23882
Db |||||
QY 3407 AATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGTTGTCTGTCGCCCTTGGCT 3466
Db |||||
QY 23883 AATCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGTTGTCTGTCGCCCTTGGCT 23942
Db |||||
QY 3467 CTATCCCTGCCACAGGTGGAACTGGAGGAGTGGGTGCAGACTTGGGTCTCTGA 3526
Db |||||
QY 23943 CTATCCCTGCCACAGGTGGAACTGGAGGAGTGGGTGCAGACTTGGGTCTCTGA 24002
Db |||||
QY 3527 CCCCGGCTTGAATTTCTTTCTAGTCTCGGGCTAGATTCGACCTTGGGTCTCTGA 3586
Db |||||
QY 24003 CCCCGGCTTGAATTTCTTTCTAGTCTCGGGCTAGATTCGACCTTGGGTCTCTGA 24062
Db |||||
QY 3587 CACAACACCATCCAAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCT 3646
Db |||||
QY 24063 CACAACACCATCCAAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCT 24122
Db |||||
QY 3647 GCCCGGCAACCCGGGCTCTCTGGGCAAGAAATGTGAGCCCTTACCCCAACCCCTTC 3706
Db |||||
QY 24123 GCCCGGCAACCCGGGCTCTCTGGGCAAGAAATGTGAGCCCTTACCCCAACCCCTTC 24182
Db |||||
QY 3707 AACTACAGAACTCTGGCCCAACCCAGCAGTATTTTAAATGTTGAGGATTTATG 3766
Db |||||
QY 24183 AACTACAGAACTCTGGCCCAACCCAGCAGTATTTTAAATGTTGAGGATTTATG 24242
Db |||||
QY 3767 AGTTATGATCAATTTGTATTAATTAAGTTAAGTTACAGATGTCA 3807
Db |||||
QY 24243 AGTTATGATCAATTTGTATTAATTAAGTTAAGTTACAGATGTCA 24283

RESULT 5

US-09-927-091-6
; Sequence 6, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45845
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-6

Query Match 20.6%; Score 788; DB 9; Length 45845;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1008; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 AGGCTGCGCTGGAACCAAGCGGTGCTGCTAGCTCGCGGGTAAAGGGTGGCGCTGGG 60
Db |||||
QY 24164 AGGCTGCGCTGGAACCAAGCGGTGCTGCTAGCTCGCGGGTAAAGGGTGGCGCTGGG 24223
Db |||||

QY 61 CCAGGTTTGGGGCGGGATCCGGCAGCTGAGCGGCGCGACCCCTCTCTTCTCTGCC 120
Db |||||
QY 24224 CCAGGTTTGGGGCGGGATCCGGCAGCTGAGCGGCGCGACCCCTCTCTTCTCTGCC 24283
Db |||||
QY 121 GGTACAGCCCAATGACGGCTCGGCTGGCTGCCCTTCCCTCCAGGATTCGCCCA 180
Db |||||
QY 24284 GGTACAGCCCAATGACGGCTCGGCTGGCTGCCCTTCCCTCCAGGATTCGCCCA 24343
Db |||||
QY 181 GCTTCTCGCCCTCCCGCACCGCCCGGATTTTCAGCCCTTTCAGGAGTTCAC 240
Db |||||
QY 24344 GCTTCTCGCCCTCCCGCACCGCCCGGATTTTCAGCCCTTTCAGGAGTTCAC 24403
Db |||||
QY 241 CCCGCTCGGGATCCCTTTCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTAGAA 300
Db |||||
QY 24404 CCCGCTCGGGATCCCTTTCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTAGAA 24463
Db |||||
QY 301 CCTCCCGTTCAGGATCTCCGCTCCCTCAGCGCTCAGAGCTCTCCAGAGCCCATGCC 360
Db |||||
QY 24464 CCTCCCGTTCAGGATCTCCGCTCCCTCAGCGCTCAGAGCTCTCCAGAGCCCATGCC 24523
Db |||||
QY 361 TTGAGCTGCCCACTTACCTCTAGACTGCCCTCCCGGGTGGGCTCCACGAGTCTCAGCC 420
Db |||||
QY 24524 TTGAGCTGCCCACTTACCTCTAGACTGCCCTCCCGGGTGGGCTCCACGAGTCTCAGCC 24583
Db |||||
QY 421 GGGACCCCTTCTCGGCTTACCTCTCCGACAGCACCCCTTCTTCGGGTAGC 480
Db |||||
QY 24584 GGGACCCCTTCTCGGCTTACCTCTCCGACAGCACCCCTTCTTCGGGTAGC 24643
Db |||||
QY 481 TCTTACCCCTTCTCGGCTTACCTCTCCGACAGCACCCCTTCTTCGGGTAGC 540
Db |||||
QY 24644 TCTTACCCCTTCTCGGCTTACCTCTCCGACAGCACCCCTTCTTCGGGTAGC 24703
Db |||||
QY 541 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 600
Db |||||
QY 24704 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 24762
Db |||||
QY 601 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 660
Db |||||
QY 24763 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 24822
Db |||||
QY 661 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 720
Db |||||
QY 24823 GCGCGCGCTCTCTCAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 24882
Db |||||
QY 721 GTGCGCAGGAGCGCGAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 780
Db |||||
QY 24883 GTGCGCAGGAGCGCGAGCGCGCCCTTCCGCTCGGCGCCCTCTCTGCTGCGCCCTGGC 24942
Db |||||
QY 781 CCGCGCTGCGCGCCAGCTTCAAGCTGGCCCAATCTGCGAGCGCTTACAGCTCTTCCCG 840
Db |||||
QY 24943 CCGCGCTGCGCGCCAGCTTCAAGCTGGCCCAATCTGCGAGCGCTTACAGCTCTTCCCG 25002
Db |||||
QY 841 CTGAGCGCCATCTCAAGCGCGCGCCAGCTGGCCCAATCTGCGAGCGCTTACAGCTCTTCCCG 900
Db |||||
QY 25003 CTGAGCGCCATCTCAAGCGCGCGCCAGCTGGCCCAATCTGCGAGCGCTTACAGCTCTTCCCG 25062
Db |||||
QY 901 AAGCTCTTCTGCTCAGCGAGCCGCGCTTCTCTGCTTCTCTGCGAGCGCTGCTGCTG 960
Db |||||
QY 25063 AAGCTCTTCTGCTCAGCGAGCCGCGCTTCTCTGCTTCTCTGCGAGCGCTGCTGCTG 25122
Db |||||
QY 961 CACGAGCAGCATCAGGTACCGGCTACGAGCGCTTTCGAGAGCTGCG 1011
Db |||||
QY 25123 CACGAGCAGCATCAGGTACCGGCTACGAGCGCTTTCGAGAGCTGCG 25173
Db |||||

RESULT 6

US-10-027-632-100265/c
; Sequence 100265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome

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; Publication No. US20030204075A9
;
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-100265

Query Match          15.0%; Score 575; DB 16; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.6e-274;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345  C A G A G T G T C C C T C C A G C C C A G C C C T G A C C T C A G A A G T G T C A G A C A T G C C A G C A G T T 2404
DB 610   C C A G T G T C C C T C C A G C C C A G C C C T G A C C T C A G A A G T G T C A G A C A T G C C A G C A G T T 551

QY 2405  G G C A G C C C G A A A G A C A C A G A C A C C C T C T T A T G T C C C A T G G C C T A A G A C T T A C C C C T G A C 2464
DB 550   G G C A G C C C G A A A G A C A C A G A C A C C C T C T T A T G T C C C A T G G C C T A A G A C T T A C C C C T G A C 491

QY 2465  C A A G C T A G T A T G A T G G C C A A T T A C C C T G A C C C C A G T C C A C A G T G T C A C A G T A G T A C C T 2524
DB 490   C A A G C T A G T A T G A T G G C C A A T T A C C C T G A C C C C A G T C C A C A G T G T C A C A G T A G T A C C T 431

QY 2525  G G T C C T A G G C T T G C C T C A G A G C C A A C C T C C T G C C A C C C C A C A C A A G A A C T A T A T G G 2584
DB 430   G G T C C T A G G G T T G C C T C A G A G C C A A C C T C C T G C C A C C C C A C A C A A G A A C T A T A T G G 371

QY 2585  T T C C T A C T T C C C A C T G A T C T G C T G A T G A T G A T G T G T G G C T G T G A A G C A C C 2644
DB 370   T T C C T A C T T C C C A C T G A T C T G C T G A T G A T G A T G T G T G G C C T G T G A A G C A C C 311

QY 2645  T G G T A G T T A G T C A C A C A T T A T A G T C A T G T G C C A C C A C C A C C T C C T G C C C A C A G C C G A G G 2704
DB 310   T G G T A G T T A G T C A C A C A T T A T A G T C A T G T G C C A C C A C C C T C C T G C C C A C A G C C G A G G 251

QY 2705  G A C A G G T G A G G T A T A C C C A A A G C C T G A T G C A G A C C C A T T A G C C T A A A A G A A C T G C A G 2764
DB 250   G A C A G G T G A G G T A T A C C C A A A G C C T G A T G C A G A C C C A T T A G C C T A A A A G A A C T G C A G 191

QY 2765  G A C A A G C C T C C C T G A T A T C A G A G T C C C A G T A G C T C T G A C A A G A G T C C A G C C A C C C 2824
DB 190   G A C A A G C C T C C C T G A T A T C A G A G T C C C A G T A G C T C T G A C A A G A G T C C A G C C A C C C 131

QY 2825  T C T T C A G C C A G C C T C T G T A C C T G C T A G G T G C A G G A G C C T T C C A G A A G C A G T T G T 2884
DB 130   T C T T C A G C C A G C C T C T G T A C C T G C T A G G T G C A G G A G C C T T C C A G A A G C A G T T G T 71

QY 2885  A A T T A G G A C C C A A G A C A T G G A G G G G C T G T T G G C T 2919
DB 70    A A T T A G G A C C C A A G A C A T G G A G G G G C T G T T G G C T 36

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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-100265

Query Match 15.0%; Score 575; DB 13; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.6e-274;
Matches 575; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 CCAGTGTCCTCCAGCCAGCCAGCCTGACCTCAGGAAGTGTACAGCATGGCCAGTAGTT 2404
DB 610 CCAGTGTCCTCCAGCCAGCCAGCCTGACCTCAGGAAGTGTACAGCATGGCCAGTAGTT 551

QY 2405 GGCAGCCGGAAGACACACAGCAGCCCTCTTATGTCCCATGGCCTTAAGACTTACCCCTGAC 2464
DB 550 GGCAGCCGGAAGACACACAGCAGCCCTCTTATGTCCCATGGCCTTAAGACTTACCCCTGAC 491

QY 2465 CAAGCTAGTGATGGCCCATTTACCCCTTGACCCAGTCCACAGTGGTCAAGGTAGTACCT 2524
DB 490 CAAGCTAGTGATGGCCCATTTACCCCTTGACCCAGTCCACAGTGGTCAAGGTAGTACCT 431

QY 2525 GGTCTTAGGGTGGCTCAGAGCCAACTCTCTGCCACCCCCACACCAAGAACTATATGG 2584
DB 430 GGTCTTAGGGTGGCTCAGAGCCAACTCTCTGCCACCCCCACACCAAGAACTATATGG 371

QY 2585 TTCCTACTTCTCCACTGATCTGTGTGTAGTGATGTGTGGCTGTGGAGGCAACC 2644
DB 370 TTCCTACTTCTCCACTGATCTGTGTGTAGTGATGTGTGGCTGTGGAGGCAACC 311

QY 2645 TGGTAGTTAGTCCACACATTTATAGTCAATGTGCCACACCTTCTCTGCCACAGCCGAGG 2704
DB 310 TGGTAGTTAGTCCACACATTTATAGTCAATGTGCCACACCTTCTCTGCCACAGCCGAGG 251

QY 2705 GACAGGGTGAGGTATACCCAAAGCTGATGACAGCCCATTTAGCCTAAAAGCAACTGCAG 2764
DB 250 GACAGGGTGAGGTATACCCAAAGCTGATGACAGCCCATTTAGCCTAAAAGCAACTGCAG 191

QY 2765 GACAGCCTCCCTGGATGATCGAGGTCCCGTAGTCTCTGAACAGAGTCCAGCCCAACC 2824
DB 190 GACAGCCTCCCTGGATGATCGAGGTCCCGTAGTCTCTGAACAGAGTCCAGCCCAACC 131

QY 2825 TCCTCAGCCAGCCCTCTGTGACCTCTAGGGTGCAGGAGGCTTCCAGAAAGCAGTTGTGT 2884
DB 130 TCCTCAGCCAGCCCTCTGTGACCTCTAGGGTGCAGGAGGCTTCCAGAAAGCAGTTGTGT 71

QY 2885 AATTAGGACCCAGCACTGGGAGGGGCTGTGGCT 2919
DB 70 AATTAGGACCCAGCACTGGGAGGGGCTGTGGCT 36

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RESULT 7
US-10-027-632-100265/c
. sequence 100265. Application US/10027632

RESULT 8
US-09-864-761-7231/c
; Sequence 7231, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 7231
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
US-09-864-761-7231
Query Match 12.9%; Score 493; DB 9; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.4e-233;
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1602 CTTGATGTGAGGTGTCGGTGTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTG 1661
DB |||||
573 CTTGATGTGAGGTGTCGGTGTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTG 514
QY 1662 GGAGTGGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACGAGCGCAAG 1721
DB |||||
513 GGAGTGGTGGTGGCGGAGAGACCCAGTGGGTGATCGGGTGGCACGAGCGCAAG 454
QY 1722 CGCAAGGGCAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGTCATCGTGCACGA 1781
DB |||||
453 CGCAAGGGCAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGTCATCGTGCACGA 394
QY 1782 TGGCAACCAGTACACGCGCTTCACGAGCCCTGGACGCGGCTTAACGTCGCGGACAAGCT 1841
DB |||||
393 TGGCAACCAGTACACGCGCTTCACGAGCCCTGGACGCGGCTTAACGTCGCGGACAAGCT 334
QY 1842 TGCAAGGTGGTGTCTTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA 1901
DB |||||
333 TGCAAGGTGGTGTCTTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA 274
QY 1902 TGACATGTCCTGGCTCTACACCTTCCGCGAGAAGTTCCTTGGCAAGCTCTGCTTACTT 1961
DB |||||
273 TGACATGTCCTGGCTCTACACCTTCCGCGAGAAGTTCCTTGGCAAGCTCTGCTTACTT 214
QY 1962 CAGCCCTGGCGAGAGCCACGCCAATGGCAAGAGCGTTTCAGCCGCTGCGGATCAACCGT 2021
DB |||||
213 CAGCCCTGGCGAGAGCCACGCCAATGGCAAGAGCGTTTCAGCCGCTGCGGATCAACCGT 154
QY 2022 CCGCATCTAGTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2081
DB |||||
153 CCGCATCTAGTCCAGGAG 94
QY 2082 GCCTTGCCCGAGGA 2094
DB |||||
93 GCCTTGCCCGAGGA 81

RESULT 9

US-09-864-761-23962/c
; Sequence 23962, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

Query Match	11.3%	Score 431;	DB 9;	Length 431;
Best Local Similarity	100.0%;	Pred. No. 1.3e-202;		
Matches 431;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1643	GTAGTGGCGTCCACTACTCTGGAGGTGCTGCTGGGAGAGACCCAGTGGGTGATCGGGC	1702		
Db	GTAGTGGCGTCCACTACTCTGGAGGTGCTGCTGGGAGAGACCCAGTGGGTGATCGGGC	372		
1703	TGGCACACGAAAGCGCAGCGCAAGGCGCAGCATCCAGATCCAGCCCGCGGCTTCT	1762		
Db	TGGCACACGAAAGCGCAGCGCAAGGCGCAGCATCCAGATCCAGCCCGCGGCTTCT	312		
371	TGGCACACGAAAGCGCAGCGCAAGGCGCAGCATCCAGATCCAGCCCGCGGCTTCT	1822		
1763	ACTGCATCGTGATGACGACGATGGCAACAGTACAGCGCTGACGAGACCCCTGACAGCGGC	252		
Db	ACTGCATCGTGATGACGACGATGGCAACAGTACAGCGCTGACGAGACCCCTGACAGCGGC	1882		
1823	TTAACGTCGGGACAGCTTGCACAGGTGGGTGCTCTCTGGACTATGACCAAGGCTTGC	192		
Db	TTAACGTCGGGACAGCTTGCACAGGTGGGTGCTCTCTGGACTATGACCAAGGCTTGC	1942		
1893	TCATCTTCTACAAGTCTCATGACATGCTCTGGCTCTACACCTTCCGCGAGAAAGTTCCTG	132		
Db	TCATCTTCTACAAGTCTCATGACATGCTCTGGCTCTACACCTTCCGCGAGAAAGTTCCTG	2002		
1943	GCAAGCTCTGCTCTTACTTTACGCCCTGGCCAGAGCACGCCAATGGCAAGAACCTTCAGC	72		
Db	GCAAGCTCTGCTCTTACTTTACGCCCTGGCCAGAGCACGCCAATGGCAAGAACCTTCAGC	2062		
2003	CGGTGGGATCAACACCGTTCGCATCTTAGTCAGGCAAGGACACACACCTTCTGGG	12		
Db	CGGTGGGATCAACACCGTTCGCATCTTAGTCAGGCAAGGACACACACCTTCTGGG			
2063	ACCATGCCAC	2073		
Db	ACCATGCCAC	1		

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; Sequence 4, Application US/09927091					
; Patent No. US20020119541A1					
; GENERAL INFORMATION:					
; APPLICANT: KILLARY, ANN					
; APPLICANT: LOTT, STEVE					
; APPLICANT: CHANDLER, DAWN					
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1					
; FILE REFERENCE: UTSC:651US					
; CURRENT APPLICATION NUMBER: US/09/927,091					
; CURRENT FILING DATE: 2001-08-09					
; PRIOR APPLICATION NUMBER: 60/227,560					
; PRIOR FILING DATE: 2000-08-23					
; PRIOR APPLICATION NUMBER: 60/225,033					
; PRIOR FILING DATE: 2000-08-10					
; NUMBER OF SEQ ID NOS: 9					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 4					
; LENGTH: 49744					
; TYPE: DNA					
; ORGANISM: Human					
US-09-927-091-4					
Query Match 3.9%; Score 149; DB 9; Length 49744;					
Best Local Similarity 99.2%; Pred. No. 4.4e-63;					
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	655	TACGAGGCCCGGTGAGCTGGCTGCGAGCACTACTTCTGCGCGCGCTGCATCACGGAG	714		
DB	34965	TACCAGGACCCCGTGAGCCTGGGCTGCGAGCACTACTTCTGCGCGCGCTGCATCACGGAG	35024		
QY	715	CAGTCGGTGGCGCAGGAGCGCAGGCGCGCGCACTGCCCGAGTCCCGCGCACGTTCC	774		
DB	35025	CACTGGTTCGCGAGGAGCGCAGGCGCGCGCACTGCCCGAGTCCCGCGCACGTTCC	35084		
QY	775	GCCGAGCCCGCGCTGGCGGCCAGCTCAAGCTGGCCAACTCTGGAGCGCTACAGCTCC	834		
DB	35085	GCCGAGCCCGCGCTGGCGGCCAGCTCAAGCTGGCCAACTCTGGAGCGCTACAGCTCC	35144		
QY	835	TTCGCGCTGGAGCGCATCTCAACGCGCGCGCGCGCACCTGCCAGGCGCACGAC	894		
DB	35145	TTCGCGCTGGAGCGCATCTCAACGCGCGCGCGCGCACCTGCCAGGCGCACGAC	35204		
QY	895	AAGGTCAAAGCT 905			
DB	35205	AAGGTCAAAGCT 35215			
RESULT 11					
US-09-908-975-16197					
; Sequence 16197, Application US/09908975					
; Publication No. US20030165843A1					
; GENERAL INFORMATION:					
; APPLICANT: SHOSHAN, Avi					
; APPLICANT: WASSERMAN, Alon					
; APPLICANT: MINTZ, Eli					
; APPLICANT: MINTZ, Ilat					
; APPLICANT: FAIGLER, Simchon					
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND					
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME					
; FILE REFERENCE: 36688-0005					
; CURRENT APPLICATION NUMBER: US/09/908,975					
; CURRENT FILING DATE: 2001-07-20					
; PRIOR APPLICATION NUMBER: US 60/287,724					
; PRIOR FILING DATE: 2001-05-02					
; PRIOR APPLICATION NUMBER: US 60/221,607					
; PRIOR FILING DATE: 2000-07-28					
; NUMBER OF SEQ ID NOS: 32337					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 16197					
; LENGTH: 60					
; TYPE: DNA					

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; ORGANISM: Homo sapiens
US-09-908-975-16197

Query Match
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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3668 CTTGGGCAAAAGGAATTGTCAGCCCTTACCCCAACCTTCACTACCAAGATCTGGCCAC 3727
Db 1 CTTGGGCAAAAGGAATTGTCAGCCCTTACCCCAACCTTCACTACCAAGATCTGGCCAC 60

RESULT 12
US-10-116-275-299/c
; Sequence 299, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Eian Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; NUMBER OF SEQ ID NOS: 202-10-04
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 299
; LENGTH: 1652
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-299

Query Match
 0.8%; Score 29; DB 16; Length 1652;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3798 ACAGTGTCTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 1474 ACAGTGTCTCAAAAAAAAAAAAAAAAAAAAAA 1446

RESULT 13
US-10-437-963-80513
; Sequence 80513, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80513
; LENGTH: 1754
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80128C.1
US-10-437-963-80513

Query Match
 0.7%; Score 27; DB 17; Length 1754;
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3800 AGATGTCTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 1728 AGATGTCTCAAAAAAAAAAAAAAAAAAAAAA 1754

RESULT 14
US-10-087-192-2014/c
; Sequence 2014, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2014
; LENGTH: 248436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(248436)
; OTHER INFORMATION: n = A, T, C or G
US-10-087-192-2014

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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3800 AGATGTCTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 187916 AGATGTCTCAAAAAAAAAAAAAAAAAAAAAA 187890

RESULT 15
US-09-969-034-4195
; Sequence 4195, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4195
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-034-4195
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us-09-927-091-3.oli15.rmpb

Mon Aug 2 10:03:35 2004

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 Best Local Similarity 100.0%; Pred. No. 0.063;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3801 GATGTCAAAAAAAAAAAAAAAAAAA 3826
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 Db 245 GATGTCAAAAAAAAAAAAAAAAAAA 270

Search completed: July 31, 2004, 12:31:55
 Job time : 1604 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 01:26:32 ; Search time 9090 seconds
(without alignments)
12569.054 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggttgctggaccgaagc.....aaaaaaaaaaaaaaaaaaaaa 3826

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 15

Total number of hits satisfying chosen parameters: 2492743

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: em_estba:*

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3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	751	19.6	835	14	CA310925
c 3	721	18.8	769	14	CA444761
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5	647	16.9	785	14	CB960090
c 6	634	16.6	634	12	BQ018441
7	634	16.6	935	13	BQ069145
c 8	632	16.5	632	12	BM994555
9	617	16.1	841	14	CF995034
10	613	16.0	664	12	BM722392
11	594	15.5	851	12	BM703589
c 12	594	15.5	931	13	BU527114
c 13	587	15.3	682	14	CA309985
c 14	582	15.2	633	12	BM994326
15	533	13.9	628	9	AU132503
16	519	13.6	519	9	AL138362
17	509	13.3	510	13	BM283437
18	508	13.3	973	13	BQ879837
c 19	489	12.8	501	9	AL138363
20	489	12.8	1018	13	BQ723205
c 21	455	11.9	470	10	AW515028
22	441	11.5	868	13	BQ069935
c 23	440	11.5	486	9	AI457621
c 24	434	11.3	451	14	CA434008
c 25	431	11.3	477	10	BE671191
c 26	427	11.2	705	10	BE258134
c 27	423	11.1	557	9	AU154016
c 28	421	11.0	423	9	AI066431
29	421	11.0	501	13	BQ187235
30	415	10.8	983	10	BE795637
c 31	405	10.6	456	10	BE856182
c 32	403	10.5	456	9	AA700789
c 33	399	10.4	502	14	CK300567
c 34	391	10.2	512	9	AI681374
35	386	10.1	507	10	BE115402
c 36	378	9.9	431	14	R71654
37	370	9.7	497	10	BE244684
38	367	9.6	998	13	BU553767
39	337	8.8	810	14	CB960174
c 40	319	8.3	424	14	CA434086
41	317	8.3	906	13	BU171407
42	305	8.0	543	14	R71157
c 43	304	7.9	304	9	AI383065
c 44	299	7.8	376	10	BE245533
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ALIGNMENTS

RESULT 1

BM457033

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
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BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

1049 bp
linear
EST 05-FEB-2002
cDNA clone IMAGE:5583269

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
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BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
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EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
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EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

BM457033
AGENCOURT_6406661 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5583269
5', mRNA sequence.
BM457033
BM457033.1 GI:18506073
EST.
Homo sapiens (human)

3166 CTCGCTGCAGAACTAGGCTCCC 3187

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Db |||
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Db |||
QY 3254 CCAATCTAAATTTTACAAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAACT 3313
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QY 571 CCAATCTAAATTTTACAAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAACT 512
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QY 3314 TGGCTGCAAGGAGTCTCGGAAATGTCATTTCCCTAGAGAAAGTGTAGGTTGGGTGAGC 3373
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QY 511 TGGCTGCAAGGAGTCTCGGAAATGTCATTTCCCTAGAGAAAGTGTAGGTTGGGTGAGC 452
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QY 3374 AAGCCCACTCTAGGTTGTCCTGCCCTTGCTCTATCCCTGCCAGAGTGGGAATCGG 3433
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QY 3674 CAAAGGAAATGTCAGCCCTACCCCACTTCACTTACAGATCTGGGCGCCACCCGAGC 3733
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QY 151 CAAAGGAAATGTCAGCCCTACCCCACTTCACTTACAGATCTGGGCGCCACCCGAGC 92
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QY 3734 AGTATTTTAAATTTGTTGCTTATGAGTTATGATCAATTTGATTAATTA 3793
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QY 3794 AGTATTTTAAATTTGTTGCTTATGAGTTATGATCAATTTGATTAATTA 32
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QY 31 AGTTACAGATGTCACAAAAA 1
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RESULT 3
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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JOURNAL
COMMENT
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FEATURES
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/dev_stage="Adult"
/lab_host="DHI10B (Life Technologies)"
/clone_lib="NCI CGAP DHI"
/note="Torgan; Lung; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DHI is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dri)18 tail. The
sequence tag for this library is AGATCATTTGC.
TAG_TISSUE=lung
TAG_LIB=UI-H-DHI
TAG_SEQ=AGATCATTTGC"
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ORIGIN

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Query Match      18.8%; Score 721; DB 14; Length 769;
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 736 GAACCTCCAGCGCCAGATTTCATCATGTCCTGTGACCAAGAACTGCCCCCATCTGCA 677
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QY 3142 GGAAGCACTATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTCTGCCACGGTCCG 3201
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QY 676 GGAAGCACTATGCCAGAAAGCTGCTGACTGCAGAACTAGGCTCCCTCTGCCACGGTCCG 617
Db |||
QY 3202 TGCCAGCAATAGATGTCCTGAGGCTGCCCTCTCCCACTTCCAGTTCAGTCCCAATCT 3261
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QY 616 TGCCAGCAATAGATGTCCTGAGGCTGCCCTCTCCCACTTCCAGTTCAGTTCAGTCCCAATCT 557
Db |||
QY 3262 AAATTTTACAGAGATTTCTGTTGGGGAACCTTAAGTCAGATCCAGAACTTGGGTGCA 3321
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QY 556 AAATTTTACAGAGATTTCTGTTGGGGAACCTTAAGTCAGATCCAGAACTTGGGTGCA 497
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QY 3322 AGGAGTCTGGGAAATGTCATTTCCCTAGAGAACTTAGGTTGGGTGGAGCAAGCCCCA 3381
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QY 496 AGGAGTCTGGGAAATGTCATTTCCCTAGAGAACTTAGGTTGGGTGGAGCAAGCCCCA 437
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QY 3382 CTGCGGTTTCTTCCACAGCATCCATCGTGAAGAACTCGGGAGAGGTGGAGTCCACA 3441
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QY 436 CTGCGGTTTCTTCCACAGCATCCATCGTGAAGAACTCGGGAGAGGTGGAGTCCACA 377
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QY 376 TCTAGGTTGTCCTGCCCTTGGCTCTATCCCTGCCAGAGTGGAACTGGAGGAGTGG 317
Db |||
QY 3502 GCTCAAGACTGAGCCTAAATGTCCTCCCGGCTTGAATTTCTTAGTCTCTGGGCT 3561
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QY 316 GCTCAAGACTGAGCCTAAATGTCCTCCCGGCTTGAATTTCTTAGTCTCTGGGCT 257
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QY 3562 TAGATTCGACTTGGGCTCTGACACACACATCCCAAAGTAGCCGGAAGAGTCA 3621
Db |||
QY 256 TAGATTCGACTTGGGCTCTGACACACACATCCCAAAGTAGCCGGAAGAGTCA 197
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QY 3622 AACACAGGGGTTCTTAAATGCTGTCCTCCCGGCTTGAATTTCTTAGTCTCTGGGCT 3681
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QY 196 AACACAGGGGTTCTTAAATGCTGTCCTCCCGGCTTGAATTTCTTAGTCTCTGGGCT 137
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5'-TTTTTTTTTTTTTTT-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."

ORIGIN

Query Match 16.9%; Score 647; DB 14; Length 785;
Best Local Similarity 99.9%; Pred. No. 8.4e-113;
Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 371 CACTACCTCTAGACTGCGCTCCCGGCTGGCGTCCACGGAGTCTCAGCCGCGCACCCCT 430
Db CACTACCTCTAGACTGCGCTCCCGGCTGGCGTCCACGGAGTCTCAGCCGCGCACCCCT 87

QY 431 TCCTTCGCGTACCTCTCTCCGACAGACACCCCTCCCTCTCCGTTAGCTCTACCCCT 490
Db TCCTTCGCGTACCTCTCTCCGACAGACACCCCTCCCTCTCCGTTAGCTCTACCCCT 147

QY 491 GCCTGTGCGGCGCTGCTCCCGCGCCCGACGCTCGGTGCTGCTCCGACAGCGCGCGCT 550
Db GCCTGTGCGGCGCTGCTCCCGCGCCCGACGCTCGGTGCTGCTCCGACAGCGCGCGCT 207

QY 551 CTCTAGCGCGCCCTGCTGCGCCCTCGGCGCCCTCTCTGCTGCGCCCTGCGCGCATGCGCT 610
Db CTCTAGCGCGCCCTGCTGCGCCCTCGGCGCCCTCTCTGCTGCGCCCTGCGCGCATGCGCT 267

QY 611 GCAGCCTCAAGGACGAGCTGCTGCTCCTATCTGCTGAGCATCTACAGGACCCCGTGA 670
Db GCAGCCTCAAGGACGAGCTGCTGCTCCTATCTGCTGAGCATCTACAGGACCCCGTGA 327

QY 671 GCCTGGGCTGCGAGCACTACTTCTGCGCGCGTGCATCAGGAGCACTGGTGGCGCAGG 730
Db GCCTGGGCTGCGAGCACTACTTCTGCGCGCGTGCATCAGGAGCACTGGTGGCGCAGG 387

QY 731 AGGCGAGGCGCGCGGAGTGCCTGCGCGCGCAGCTTTCGCGAGCGCGCGCTGG 790
Db AGGCGAGGCGCGCGGAGTGCCTGCGCGCGCAGCTTTCGCGAGCGCGCGCTGG 447

QY 791 CGCCCAAGCTCAAGCTGCGCAACATCGTGGAGCGCTACAGCTCTCTCCGCTGGACGCA 850
Db CGCCCAAGCTCAAGCTGCGCAACATCGTGGAGCGCTACAGCTCTCTCCGCTGGACGCA 507

QY 851 TCCTCAAGCGCGCGCGCGGCGGACCTGCGAGCGCACACAGGTCAGGCTCTTCT 910
Db TCCTCAAGCGCGCGCGCGGCGGACCTGCGAGCGCACACAGGTCAGGCTCTTCT 567

QY 911 GCCTCAGGACCGCGGCTTCTGCTTCTTCTGCGAGCGGCTGCACTGCGAGCAGC 970
Db GCCTCAGGACCGCGGCTTCTGCTTCTTCTGCGAGCGGCTGCACTGCGAGCAGC 627

QY 971 ATCAGCTCACCGGCTCAGACGAGCTTCCGAGCTGCGAGGAGCTGAGGACCAAC 1030
Db ATCAGCTCACCGGCTCAGACGAGCTTCCGAGCTGCGAGGAGCTGAGGACCAAC 687

QY 1031 TTCAGGCGCTTCAAGACAGCGAGCGGGAACACACCGAA 1068
Db TTCAGGCGCTTCAAGACAGCGAGCGGGAACACACCGAA 725

RESULT 6

BQ018441/c
LOCUS
DEFINITION
IMAGE:5893122 3', mRNA sequence.
ACCESSION
BQ018441

BQ018441
UI-H-DH1-awq-p-19-0-UI-s1 NCI_CGAP_DHI Homo sapiens cDNA clone
EST 17-JUN-2002
linear
634 bp mRNA

VERSION BQ018441.1 GI:19753718
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 634)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5893122"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_DHI"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP DHI is a normalized cDNA library containing the
following tissue(s): VS-8 Cell line from Metastatic
Chondrosarcoma in Lung. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dr primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AGATCATTCG.
TAG TISSUE=Lung
TAG LIB=UI-H-DHI
TAG_SEQ=AGATCATTCG"

ORIGIN

Query Match 16.6%; Score 634; DB 12; Length 634;
Best Local Similarity 100.0%; Pred. No. 2.8e-110;
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3191 GCCAGGTCGCGCCAGCAATAGATGCTGAGCGCTGCCCTCTCCACATCACTCAG 3250
Db GCCAGGTCGCGCCAGCAATAGATGCTGAGCGCTGCCCTCTCCACATCACTCAG 634

QY 3251 TTCCCAATCTAAATTTTACAGAGATTTCTTTGGGGGAACTTAAGTCAGATCCAGAA 3310
Db TTCCCAATCTAAATTTTACAGAGATTTCTTTGGGGGAACTTAAGTCAGATCCAGAA 515

QY 3311 CTTGGCTGCAAGGGAGTCTGGAAATGTCATTTCCCTAGAAGGAAGTTAGGGTGGGTGG 3370
Db CTTGGCTGCAAGGGAGTCTGGAAATGTCATTTCCCTAGAAGGAAGTTAGGGTGGGTGG 455

QY 3371 AGCAAGCCCACTCCGTTTCTGCCACAGATCCAAATCGTGAAGAACTCGGGAGAGGG 3430
Db AGCAAGCCCACTCCGTTTCTGCCACAGATCCAAATCGTGAAGAACTCGGGAGAGGG 395

QY 3431 TGGAGTCCACATCTAGGGTCTCTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAAC 3490
Db TGGAGTCCACATCTAGGGTCTCTCTGCCCTTGGCTCTATCCCTGCCAGAGGTGGGAAC 335

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

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Location/Qualifiers
1. .632
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5871536"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DH0"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site 2: Not I; NCI CGAP DH0 is a cDNA library containing the following tissues": VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is AGATCATGTC.
TAG TISSUE=lung
TAG LIB=VI-H-DH0
TAG SEQ=AGATCATGTC"

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ORIGIN

Query Match	16.5%; Score 632; DB 12; Length 632;	
Best Local Similarity	100.0%; Pred. No. 6.7e-110;	
Matches 632; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;	
QY	3193	CACGGTCCGTGCAGAGCAATAGATGTCCTGAGGCCTGCCCTCTCCACATTCCTCAGTT 3252
Db	632	CACGGTCCGTGCAGAGCAATAGATGTCCTGAGGCCTGCCCTCTCCACATTCCTCAGTT 573
QY	3253	CCCAATCTAAATTTTACAAGAGATCTGTGTGGGGGAACTTTAAGTCAGATCCAGAACC 3312
Db	572	CCCAATCTAAATTTTACAAGAGATCTGTGTGGGGGAACTTTAAGTCAGATCCAGAACC 513
QY	3313	TTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGAGAGAGTTAGGTGGGTGGAG 3372
Db	512	TTGGCTGCAAGGAGTCTGGGAAATGTCATTTCCCTAGAGAGAGTTAGGTGGGTGGAG 453
QY	3373	CAAGCCCACTGGTTTTTCTGCCACAGCATCCAATCTGTAAGAACTCGGAGAGGGTG 3432
Db	452	CAAGCCCACTGGTTTTTCTGCCACAGCATCCAATCTGTAAGAACTCGGAGAGGGTG 393
QY	3433	GAGTCCACATCTAGGGTTGCTCTGCCCTTGCTCTATCCCTGCCAGAGGTGGGAATCG 3492
Db	392	GAGTCCACATCTAGGGTTGCTCTGCCCTTGCTCTATCCCTGCCAGAGGTGGGAATCG 333
QY	3493	GAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCCTTGACATTTCTTTCTAGT 3552
Db	332	GAGGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCCCGGCCTTGACATTTCTTTCTAGT 273
QY	3553	CCTGGGGCTAGATTCTGCATTTGGGTCTCTGCACACACACACATCCCAAGTAGCG 3612
Db	272	CCTGGGGCTAGATTCTGCATTTGGGTCTCTGCACACACACACATCCCAAGTAGCG 213
QY	3613	GAAGAGCTAAACAAGGGGGTTCTTAAATGGCTGCCCGCCGACCCGGGGCTCCCTGG 3672


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QY 911 GCCTCAGGACCGCGGCTTCTCTCTTCTTCTGACGAGCCTGCACTGCACGAGCAGC 970
Db 601 GCCTCAGGACCGCGGCTTCTCTCTTCTTCTGACGAGCCTGCACTGCACGAGCAGC 660
QY 971 ATCA 974
Db 661 ATCA 664

RESULT 11
BG703589 851 bp mRNA linear EST 07-MAY-2001
LOCUS 602686426F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4818775 5',
DEFINITION mRNA sequence.
ACCESSION BG703589
VERSION BG703589.1 GI:13976072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0721 row: d column: 08
High quality sequence stop: 765.
FEATURES
Location/Qualifiers
1..851
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4818775"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH MGC Library."

QY 666 GGTGAGCTGGCTCGAGCACTACTTCTGCGCGCTGCATCAGGAGCACTGGGTGG 725
Db 117 GGTGAGCTGGCTCGAGCACTACTTCTGCGCGCTGCATCAGGAGCACTGGGTGG 176
QY 726 GCAGAGCGGAGGCGCGCGGAGTCCCGAGTCCGCGGCACTGCGGAGCCGCG 785
Db 177 GCAGAGCGGAGGCGCGCGGAGTCCCGAGTCCCGGCGCACTTTCGCGGAGCCGCG 236
QY 786 GCTGCGCGCCAGCTCAAGCTGGCCCAACATCGTGGAGGCTACAGCTCTTCCCGCTGGA 845

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Db 237 GCTGGGGCCAGCCCTCAAGCTGGCCCAACATCGTGGAGCGCTACAGCTCTTCCCGCTGA 296
QY 846 CCGCATCTCTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 905
Db 297 CGCCATCTCTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356
QY 906 CTTTGTGCTCAGCGGACCGCGCGCTTCTCTGTCTTCTTCTGCGACGAGCCTGCACTGCACGA 965
Db 357 CTTTGTGCTCAGCGGACCGCGCGCTTCTCTGTCTTCTTCTGCGACGAGCCTGCACTGCACGA 416
QY 966 GCAGCATCAGGTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1025
Db 417 GCAGCATCAGGTCAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 476
QY 1026 CCAACTTCAGGCGCCCTTCAAGACAGCGAGCGGGAACACACCGGAGCGCTGCACTGCTCAA 1085
Db 477 CCAACTTCAGGCGCCCTTCAAGACAGCGAGCGGGAACACACCGGAGCGCTGCACTGCTCAA 536
QY 1086 CGGACAACTGCGGAGACCAAGTCTTCCACCAAGAGCGCTGCGGACCACTATCGGCGAGGC 1145
Db 537 GCGACAACTGCGGAGACCAAGTCTTCCACCAAGAGCGCTGCGGACCACTATCGGCGAGGC 596
QY 1146 CTTGAGCGGCTGCACCGCGCTGCTGCTGAACGCGGAGCGCGCGCGCGCGCGCGCGCGCG 1205
Db 597 CTTGAGCGGCTGCACCGCGCTGCTGCTGAACGCGGAGCGCGCGCGCGCGCGCGCGCGCG 656
QY 1206 GCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1259
Db 657 GCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710

RESULT 12
BG527114
LOCUS AGENCOURT 10155963 NIH_MGC_101 Homo sapiens cDNA clone
DEFINITION IMAGE:6536868 5', mRNA sequence.
ACCESSION BG527114
VERSION BG527114.1 GI:22837555
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2698 row: o column: 12
High quality sequence stop: 552.
FEATURES
Location/Qualifiers
1..931
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536868"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

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ORIGIN

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Query Match 15.5%; Score 594; DB 12; Length 851;
Best Local Similarity 100.0%; Pred. No. 7e-103;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES	
source	

source

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1. 682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-F1-F1-bid-j-07-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP F1"
/clone="Organ: Lung; Vector: p7713-Pac;
modified polylinker; Site_1: EcoR I;
NCI_CGAP F1" is a normalized cDNA library
a pool of 81 RNA samples from Alveolar
challenged with different treatments.
normalized according to Bonaldo, Lennarsson
Research, 6:791-806, 1996. First strand
primed with an oligo-dT primer containing
Double stranded cDNA was ligated to a
digested with Not I, and cloned directly
p7713-Pac vector. The oligonucleotide
synthesis of first-strand cDNA containing
sequence that is located between the
(dT)18 tail. The sequence tag for this
GGCATGCGC. The tissue was provided by
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macroph
TAG LIB=UI-H-F1
TAG_SEQ=GGCATGCGC"

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ORIGIN

Query Match	15.3%	Score 587	DB 14	Length 682	
Best Local Similarity	100.0%	Pred. No. 1.8e-101			
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DB	607	TGAGGCTGCCCTCTCCACATTCAC	TGAGGCTGCCCTCTCCACATTCAC	TGAGGCTGCCCTCTCCACATTCAC	TGAGGCTGCCCTCTCCACATTCAC
QY	3281	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT
DB	547	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT	TGTTTGGGGAACTTAAAGTCAGAT
QY	3341	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG
DB	487	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG	ATTTCCCTAGAGAACTTAAAGTCAG
QY	3401	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG
DB	427	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG	GCATCCAACTCGTGAAGAACTCGG
QY	3461	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT
DB	367	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT	TTGGCTCTATCCCTGCCACAGAGT
QY	3521	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT
DB	307	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT	ATGTCCTCCCGGCTTGACTTTCTT
QY	3581	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA
DB	247	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA	CTCTGACACACACACACATCCAA
QY	3641	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG
DB	187	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG	ATGGCTTGCCCGCCGCAACCGGG
QY	3701	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA
DB	127	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA	CCCTTCAACTACAGAACTCGGGCA
QY					
DB					

Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

Query Match	15.5%;	Score 594;	DB 13;	Length 931;
Best Local Similarity	100.0%;	Pred. No. 6.4e-103;	Indels	0;
Matches 594;	Conservative	0;	Mismatches	0;
QY	2118	CCACCGTGGCCACTGGAGACCTCAGGCCAGTCTTTTACCTCCAGCTCCAGTCTGTAA	2177	
Db	19	CCACCGTGGCCACTGGAGACCTCAGGCCAGTCTTTTACCTCCAGCTCCAGTCTGTAA	78	
QY	2178	ATGAGAGTTGCATTTCCCTACTTTCCTAACTCTCTTCAGCATCGATGTTCTGTAGCTCTG	2237	
Db	79	ATGAGAGTTGCATTTCCCTACTTTCCTAACTCTCTTCAGCATCGATGTTCTGTAGCTCTG	138	
QY	2238	ACCTTGATAGGATACAGCTTTGATCAAGATGTGACATGGCTTCTCTCCTCAGGCCAAC	2297	
Db	139	ACCTTGATAGGATACAGCTTTGATCAAGATGTGACATGGCTTCTCTCCTCAGGCCAAC	198	
QY	2298	CCTGCCCAACCTCATCCCCATCTTCTCAGGGCAGGGAGCTACCTTCCAGTGTCTCCCT	2357	
Db	199	CCTGCCCAACCTCATCCCCATCTTCTCAGGGCAGGGAGCTACCTTCCAGTGTCTCCCT	258	
QY	2358	CCAGCCAGCCCTGACCTCAGGAAGTGTACAGCATGCCAGTAGTTGGCAGCCCGAAG	2417	
Db	259	CCAGCCAGCCCTGACCTCAGGAAGTGTACAGCATGCCAGTAGTTGGCAGCCCGAAG	318	
QY	2418	ACACACAGACCTCTTATGTGCCATGGCTTAAGACTTTACCCCTGACCAAGCTAGTGATG	2477	
Db	319	ACACACAGACCTCTTATGTGCCATGGCTTAAGACTTTACCCCTGACCAAGCTAGTGATG	378	
QY	2478	GGCCATTTACCTTGACCCCGATCCACAGTGTGTACAGTAGTACTTGCTCTAGGGTTG	2537	
Db	379	GGCCATTTACCTTGACCCCGATCCACAGTGTGTACAGTAGTACTTGCTCTAGGGTTG	438	
QY	2538	CCTGAGAGCAACCTCTCTGTGCCACCCACACCAAGAACTATATGTTCTTACTTCTCC	2597	
Db	439	CCTGAGAGCAACCTCTCTGTGCCACCCACACCAAGAACTATATGTTCTTACTTCTCC	498	
QY	2598	CACTGATCTGTGTTCAAGTAGATGCTGTGGCCCTGTGGAGGCCACTTGTTAGTTGAGTC	2657	
Db	499	CACTGATCTGTGTTCAAGTAGATGCTGTGGCCCTGTGGAGGCCACTTGTTAGTTGAGTC	558	
QY	2658	CACACATTATAGTCATGTGCCACCACTTCTTGCCACAGGCCGAGGGACAGG	2711	
Db	559	CACACATTATAGTCATGTGCCACCACTTCTTGCCACAGGCCGAGGGACAGG	612	

RESULT 13	CA309985	682 bp	mrna	linear	EST 01-NOV-2002
CA309985/c	UT-H-FT1-bid-j-07-0-UI.s1	NCI CGAP FTL	Homo sapiens	CDNA clone	
LOCUS	UT-H-FT1-bid-j-07-0-UI 3'	mrna sequence.			
DEFINITION	CA309985				
ACCESSION	CA309985.1	GI:24473039			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 682)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
JOURNAL	Tumor Gene Index				
COMMENT	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-re@mail.nih.gov				
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I				
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Clone distribution information can be obtained				

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QY 3761 TTTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGTCA 3807
DB |||||
67 TTTATGAGTTATGATCAATTTCTATTAAATTAAGTTACAGATGTCA 21
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RESULT 14
LOCUS BM994326/c
DEFINITION UI-H-DH0-aul-k-14-0-UI-s1 NCI CGAP_DH0 Homo sapiens cDNA clone
IMAGE:5871109 3', mRNA sequence.
ACCESSION BM994326
VERSION BM994326.1 GI:19719227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 633)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.

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modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP DH0 is a cDNA library containing the following
tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
in Lung. The library was constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pTT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGATCATTCG.
TAG TISSUE=lung
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 1.6e-100;
Matches 632; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB |||||
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DB |||||
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DB |||||
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DB |||||
213 GGAAGAGCTAAACACAGGGGTTCTTAAATGGCTGCCCGGCCACCGGGCTCCCTTG 154
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DB |||||
153 GGCAAAAGGAATGTTCAGCCCTACCCCAACCTTCAACTACCAATCTGGGCCACCCCA 94
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DB |||||
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QY 3792 AAAGTTACAGATGTCAAAAAAATAAAAAA 3824
DB |||||
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DEFINITION AU132503 NT2RP3 Homo sapiens cDNA clone NT2RP3004617 5', mRNA
sequence.
ACCESSION AU132503
VERSION AU132503.1 GI:10992857
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Mon Aug 2 10:03:36 2004

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ORIGIN

Query Match 13.9%; Score 533; DB 9; Length 628;
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Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 430 TTCTCGCGTTACCTCTTCCGACAGACCCCTCCCTTCTCCGGTAGCTCCTACCCC 489
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QY 610 TGCAGCCTCAAGGACGAGCTGTGTCTTCCATCTGCTGAGCATCTACAGGACCCGGTG 669
Db 241 TGCAGCCTCAAGGACGAGCTGTGTCTTCCATCTGCTGAGCATCTACAGGACCCGGTG 300

QY 670 AGCCTGGGCTCGAGCACTTCTGCGCGCGCTGCAATCAGGAGCACTGGTGGGCGAG 729
Db 301 AGCCTGGGCTCGAGCACTTCTGCGCGCGCTGCAATCAGGAGCACTGGTGGGCGAG 360

QY 730 GAGCGCAGGGCGCGCGGAGCTGCGCGAGTGCAGCGCGAGCTTCCGCGAGCGCGCTG 789
Db 361 GAGCGCAGGGCGCGCGGAGCTGCGCGAGTGCAGCGCGAGCTTCCGCGAGCGCGCTG 420

QY 790 GCGCCAGCCTCAAGCTGGCCAACTCGTGAGCGCTACAGCTCCTTCCGCTGACGCC 849
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Search completed: July 31, 2004, 08:29:15
Job time : 9098 secs

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ORIGIN

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121	TGCTGTGGGGCTCGTCCCGCGCCAGCCCTCGGTGCTCCGACAGCGCGCGC 180
550	TCTCTCAGCGCCGCCCTCGGCCGCCCTCTCTGCTGCCCCCTGGCGCCATGGCG 609
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790	GCGCCAGGCTTAAGTGGCCAACTCTGGAGCGCTACAGCTCTTCCCGCTGGACGCC 849
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910	TGCTCAAGGACCGCGCGCTTCTCTGCTTCTTGGGAAGGCTGCACTGCAAGCGCAG 969
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RESULT 3			
BD156501		3436 bp DNA linear	PAR 17-JAN-2003
LOCUS		Primer for synthesizing full-length cDNA and use thereof.	
DEFINITION			
ACCESSION	BD156501		
VERSION	BD156501.1	GI:27862259	
KEYWORDS	JP 2002191363-A/11344		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS	Ota, I., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 11344 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/11344 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC C12P21/02, C12Q1/68//C12P21/08, C06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (235) . (1659) .		

FT CDS (235). (1659).

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AK001621
AK001621.1 GI:7022986
oligo capping; fis (full insert sequence).
Homo sapiens (human)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K.,
Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y.,
Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K.,
Masuko, Y. and Kanehori, K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3436)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5' & 3' end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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CDS

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BC001222 3259 bp mRNA linear PRI 04-OCT-2003
Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone
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ACCESSION BC001222
VERSION BC001222.1 GI:12654758
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3259)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stietz, R.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrams, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
2 (bases 1 to 3259)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAL Plate: 6 Row: J Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 8922647.

FEATURES

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[illegible]

RESULT 6
BC007999
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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Homo sapiens hypothetical protein FLJ10759, mRNA (cdna clone
MGC:15757 IMAGE:3357436), complete cds.
BC007999
BC007999.1 GI:14124949
MGC.

SOURCE
ORGANISM
REFERENCE
AUTHORS

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg, R., Feingold, D.A., Grouse, L.H., Derge, J.G.,
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Altschul, S.F., Zeeberg, B., Buotow, K.H., Buetow, K.H., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heise, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaeetz, T.E., Brownstein, M.J., Ustin, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.R., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallum, D.E.,
Schnier, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
MEDLINE
PUBMED

2388257
12477932

REFERENCE
AUTHORS

2 (bases 1 to 3259)
Strausberg, R.
Direct Submission
Submitted (15-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Fawan Pandoh, Anna-Tilisa Prabhu, Parvanah Saedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Narasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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ORIGIN

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Db	1 CCTGGGCCCCCTCTGTGTCGCCCTCGGCGCCATGCGTGACGCTCAAGAGCGAGCTG				60
Qy	631 CTGTGCTCCATCTGCTGAGCATCTACAGAACCCGCTGAGCTGGGCTCGGAGCACTAC				690
Db	61 CTGTGCTCCATCTGCTGAGCATCTACAGAACCCGCTGAGCTGGGCTCGGAGCACTAC				120
Qy	691 TTCTGCGCCCTGTCATCAGGAGCATCTGGGTGGCGAGGAGCGAGGCGCGCGCGCAC				750
Db	121 TTCTGCGCCCTGTCATCAGGAGCATCTGGGTGGCGAGGAGCGAGGCGCGCGCGCAC				180
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Db	181 TGSCCCGAGTGGCGGCGCACGTTGCGCGAGCCCGCTGCGCGCCAGCTCAAGCTGGCC				240
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DB	REMARK	COMMENT
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3451	QY	Tissue Procurement: ARCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@hgr.nih.gov
2879	DB	Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
3511	QY	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: b Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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3059	DB	misc_feature 445. .798 /gene="FLJ10759" /note="BBC; Region: B-Box C-terminal domain" /db_xref="CDD:smart00502"
3691	QY	misc_feature 913. .1074 /gene="FLJ10759" /note="PRY; Region: associated with SPRY domains" /db_xref="CDD:smart00589"
3119	DB	misc_feature 1075. .1413 /gene="FLJ10759" /note="SPRY; Region: Domain in SPla and the Ryanodine
3751	QY	FEATURES
3179	DB	source
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3239	DB	BC011689 Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone MGC:19672 IMAGE:3353034), complete cds.
RESULT 7		
BC011689		
LOCUS		
DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		

Receptor."		/db_xref="CDD:smart00449"	
ORIGIN			
Query Match		84.5%; Score 3232; DB 9; Length 3259;	
Best local Similarity		99.9%; Pred. No. 0;	
Matches 3254; Conservative		0; Mismatches 0; Indels 2; Gaps 2;	
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QY	631	CTGTGCTCCATCTGCTGAGCATCTACACGACCCGGTGAGCTTGGCTGCGAGCACTAC	690
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QY	691	TTCTGCCGCCCTGTCATCACGGAGCACTGGTGCGGAGGAGGCGCAGGGCGCCCGCAC	750
Db	121	TTCTGCCGCCCTGTCATCACGGAGCACTGGTGCGGAGGAGGCGCAGGGCGCCCGCAC	180
QY	751	TGCCCGAGTGCCGGCGCACGTTTGGCGAGCCGGCTGGCGGCCAGCTCAAGCTGACC	810
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QY	811	AACATCGTGGAGCGCTACAGCTCTTCCGCTGGAOGCAATCTCAACGCGCGCGCGCC	870
Db	241	AACATCGTGGAGCGCTACAGCTCTTCCGCTGGAOGCAATCTCAACGCGCGCGCGCC	300
QY	871	GCGCGACCTTGCCAGGCGCAGCAAGGTCAAGCTTCTTCTGCTTCAAGCTGCGCTT	930
Db	301	GCGCGACCTTGCCAGGCGCAGCAAGGTCAAGCTTCTTCTGCTTCAAGCTGCGCTT	360
QY	931	CTCTGCTTCTTCTGCGAGCGCTGCACTGCAGCAGCAGCATCAGTCAAGCTGCGCTT	990
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QY	991	GAGCGCTTGCAGAGCTGCGAGGAGCTGAAGCAACCTTCAAGGCGCTTCAAGCAGC	1050
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QY	1051	GAGCGGGAACACACCGAAGCGCTGAGCTGCTCAAGGCAACCTGCGGAGACCAAGTCT	1110
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QY	1231	GACATCGAGCAGAAAGTCCAGCGCTACAGCAGCAGCTGCGCAAGTCCAGGAGGAGCC	1290
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QY	1351	TCACCTGTCGAGCGGCTCAAGGGAATAATCCATGAGACCAACCTCACATATGAAGACTTC	1410
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QY	1411	CCGACCTCCAAAGTACACAGGCGCCCTGAGTACACCATCTGGAAGTCCCTGTTCCAGGAC	1470
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QY	1531	CTGTGCGGACGACTGCACCAATTGGCTTACGGCAACTTGGACCCACAGCCACTGCAGGAC	1590
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QY	1591	TCGCCAAAGCGCTTCGATGTGAGGTGTGGTGTGGTGTCTGAAGCCCTTCAGTAGTGGC	1650
Db	1021	TCGCCAAAGCGCTTCGATGTGAGGTGTGGTGTGGTGTCTGAAGCCCTTCAGTAGTGGC	1080
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QY	1831	CGGACCAAGCTTGAACAGGTGGGTGTCTTCTGCACTATGACCAAGGCTTCCCTGCAAGCTC	1890
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Db	1321	TACATGCTGATGACATGTCTGCTCTACACCTTCCGCGAGAGTTCCTTGGCAAGCTC	1380
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QY	2311	CATCCCTTCTTCTCAGGCGAGGAGCTACCTTCCAGTGTCTCCTTCCAGCCCGAGCT	2370
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QY	2371	GACCTCAGGAGTGTTCAGAGCATGCGCAGTAGTGGAGCGCCGAGAGACACAGACACC	2430
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Db	1919	TGACCCAGTCCAGTGTTCACAGGTAGTACCTTGGTCTTAGGGTTCCTGAGAGCCAAAC	1978
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3751	QY	TGTTGCCATTTTATGAGTTATGATCAATTTGTTATTAATTAAGTTACAGATGTCAAA	3810
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BC012152 3259 bp mRNA linear PRI 04-OCT-2003
LOCUS Homo sapiens hypothetical protein FLJ10759, mRNA (cDNA clone
MGC:20370 IMAGE:4558639), complete cds.

ACCESSION BC012152
VERSION BC012152.1
KEYWORDS GI:15082475
SOURCE MGC.
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 3259)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramsen, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
Morken, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fancy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3259)
Strausberg, R.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Suzanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Nataaja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>

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RESULT 9

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Accession	AX775831		
Definition	Sequence	101	from Patent WO03048202.
Locus	AX775831		
Size	3243 bp		mRNA
Linear			
Patent	14-JUL-2003		

KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AX775831	3243 bp	mRNA	linear	PAT 14-JUL-2003
Sequence	101	from Patent WO03048202.		

. Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AX775831
AX775831.1 GI:32693549

Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Matsuda A and Muramatsu S.

NF-kB activating gene
 Patent: WO 03048202-A 101 12-JUN-2003;

Asahi Kasei Kabushiki Kaisha (JP)
Location/Qualifiers

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ORIGIN

Query Match 84.0%; Score 3212; DB 6; Length 3243;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3234; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
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Qy	2521	ACCTGGTCCTAGGGTGGCTGAGAGCCAACTCTCTGTCACCCAGTCCACAGTGGTGCACAGGTAGT	2580	Qy	1789	CAGTACAGCGCTGCAC	CGGAGC	CTTGAACGTCGGGCAAGCTTGAACAG	1848
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ACCESSION	AX491283.1	GI:22323984							
VERSION	Homo sapiens (human)								
KEYWORDS	Homo sapiens								
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	Killary, A., Chandler, D. and Lott, S.								
AUTHORS	The tumor suppressor car-1								
TITLE	Patent: WO 0212285-A 7.14-FEB-2002;								
JOURNAL	BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)								
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				Db	13619	ACCAAGACTATATGTTCTTCTTCTCCCACTGATCTGCTGTGTGATGATGATGCTGTG	13678		

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SEQUENCE, 4 unordered pieces.
AC022262
VERSION AC022262.4 GI:8569825
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 164950)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164950)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 16, 2000 this sequence version replaced gi:7321934.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H NH0150F21
----- Summary Statistics -----
Sequencing vector: M13; 75%
Chemistry: Dye-primer ET; 75% of reads
Assembly: Dye-terminator Big Dye; 25% of reads
Consensus quality: 163188 bases at least Q40
Consensus quality: 163696 bases at least Q30
Consensus quality: 163935 bases at least Q20
Insert size: 172000; agarose-fp
Quality coverage: 7.83 in Q20 bases; agarose-fp
Quality coverage: 8.20 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
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* 1 8662: contig of 8662 bp in length
* 8663 8762: gap of unknown length
* 8763 27020: contig of 18258 bp in length
* 27021 27120: gap of unknown length
* 27121 78035: contig of 50915 bp in length
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FEATURES
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RESULT 13
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ACCESSION AL662907
VERSION AC026053
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Van Hellmond, Z.
Direct Submission
Submitted (18-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:20145349.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
Rpl1-131M11 is from the library RPl1-11.1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
Draft Sequence Produced by Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
http://genome.wustl.edu/gsc/index.shtml.

FEATURES
source

Location/Qualifiers
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ORIGIN

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 ORGANISM

REFERENCE
 AUTHORS
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 136095)
 Wen, G., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N.,
 Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A.,
 Siebert, R., Taudien, S., Schilabel, M.B., Schlegelberger, B.,
 Siebert, R., Rosenthal, A. and Platzner, M.
 Chromosome 8 genomic sequence

Unpublished
 2 (bases 1 to 136095)
 Polley, A., Nordiek, G., Schlegelberger, B., Drescher, B., Weber, J.,
 Schattevooy, R. and Rosenthal, A.
 Direct Submission
 Submitted (21-JUN-1999) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
 On Oct 24, 2001 this sequence version replaced gi:14277237.

----- Genome Center
 Center: Institute of Molecular Biotechnology
 Center code: IMB
 Web site: <http://genome.imb-jena.de/>
 Contact: gsj-submit@genome.imb-jena.de
 ----- Project Information
 Center project name: H176
 Center clone name: CTA-392H5
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 Sequencing vector: M13; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 122353 bases at least Q40
 Consensus quality: 127794 bases at least Q30
 Consensus quality: 131293 bases at least Q20
 Quality coverage: 5.82 x in Q20 bases; sum-of-contigs

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality 10.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 1902: gap of unknown length
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FEATURES
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Db	67459	GCCTAAAGCACTGAGGACAGGCTCCTCGATGATCGAGTCCCACTAGCTCTGAA	67518
QY	2807	CAAGAGTCCAGCAACCTCTTCCAGCCGCTCTGTGACCTGTAGGTCAGGAGGCT	2866
Db	67519	CAAGAGTCCAGCAACCTCTTCCAGCCGCTCTGTGACCTGTAGGTCAGGAGGCT	67578
QY	2867	TCCAGAGCAGTGTGTAAATTAGACCCCAAGCACTGGAGGGGCTGTGGCTAGACCCC	2926
Db	67579	TCCAGAGCAGTGTGTGTAAATTAGACCCCAAGCACTGGAGGGGCTGTGGCTAGACCCC	67638
QY	2927	TGTGACAGTGGCATCTATCTCAGTATAGATCTCTGCTGCAGAAAACAGAGCCACTTGT	2986
Db	67639	TGTGACAGTGGCATCTATCTCAGTATAGATCTCTGCTGCAGAAAACAGAGCCACTTGT	67698
QY	2987	AGCTGTTTAAATTAGACAGGATTTACTACCTGGCCCTGTGGCTTGCAAAATTGTTGG	3046
Db	67699	AGCTGTTTAAATTAGACAGGATTTACTACCTGGCCCTGTGGCTTGCAAAATTGTTGG	67758
QY	3047	AAGAGCTGGAGAGCAGACTCTGTGAAATTTCCAGGAACCTCCAGCGCCAGATTCATCAT	3106
Db	67759	AAGAGCTGGAGAGCAGACTCTGTGAAATTTCCAGGAACCTCCAGCGCCAGATTCATCAT	67818

QY	3107	GTCTGTTGTGACCGAGAAAGCTGCCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGC	3166
Db	67819	GTCTGTTGTGACCGAGAAAGCTGCCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGC	67878
QY	3167	TGACTGCAAGAACTAGGCTCCCTCTGCGACAGGTCGTCGCGAGCAATAGATGTCCTGAGGC	3226
Db	67879	TGACTGCAAGAACTAGGCTCCCTCTGCGACAGGTCGTCGCGAGCAATAGATGTCCTGAGGC	67938
QY	3227	CTGCCCTCTCCCACTTCCACTCAGTTCCTCAAAATCTTAAATTTTCAAGAGATTCGTTTG	3286
Db	67939	CTGCCCTCTCCCACTTCCACTCAGTTCCTCAAAATCTTAAATTTTCAAGAGATTCGTTTG	67998
QY	3287	GGGAAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGCTCAATTTCC	3346
Db	67999	GGGAAACTTAAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGCTCAATTTCC	68058
QY	3347	CTAAGAGGAGTAAAGTGGGTGGAGCAAGCCCACTGCGTCAAGGGAGTCTGGGAAATGCTCAATTTCC	3406
Db	68059	CTAAGAGGAGTAAAGTGGGTGGAGCAAGCCCACTGCGTCAAGGGAGTCTGGGAAATGCTCAATTTCC	68118
QY	3407	AATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGTTGTCTGCTGCCCTTGCT	3466
Db	68119	AATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGTTGTCTGCTGCCCTTGCT	68178
QY	3467	CTATCCCTGCCAGAGGTGGAACTGGAGAGTGGGCTGCAAGACTGAGCTTAAATGCT	3526
Db	68179	CTATCCCTGCCAGAGGTGGAACTGGAGAGTGGGCTGCAAGACTGAGCTTAAATGCT	68238
QY	3527	CCCCGGCTTTGACTTTCTTTCTAGTCTGGGCTTGAATCTGCACTTGGGCTCTCTGA	3586
Db	68239	CCCCGGCTTTGACTTTCTTTCTAGTCTGGGCTTGAATCTGCACTTGGGCTCTCTGA	68298
QY	3587	CACAACACACCATCCCAAGTAGCCGAGAGCTTAAACACAGGGGTCTTTAAATGGCT	3646
Db	68299	CACAACACACCATCCCAAGTAGCCGAGAGCTTAAACACAGGGGTCTTTAAATGGCT	68358
QY	3647	GGCCCCGCCACCCGGGCTCCCTTGGGCAAAAGAAATTTGTCAGCCCTTACCCCAACCTTC	3706
Db	68359	GGCCCCGCCACCCGGGCTCCCTTGGGCAAAAGAAATTTGTCAGCCCTTACCCCAACCTTC	68418
QY	3707	AATACCCAGAACTGGGCCACCCAGCAGTATTTTAAATTTTAAATTTGCCCCATTTATG	3766
Db	68419	AATACCCAGAACTGGGCCACCCAGCAGTATTTTAAATTTTAAATTTGCCCCATTTATG	68478
QY	3767	AGTTATGATCAATTTGTAATTAATTAAGTTACAGATGTCA	3807
Db	68479	AGTTATGATCAATTTGTAATTAATTAAGTTACAGATGTCA	68519

Search completed: July 31, 2004, 16:55:09
Job time : 14411 secs

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Result No.	Query No.	Score	Query			DB	ID	Description
			Match	Length	%			
1	1	3826	100.0	3826	6	ABK12806	ABK12806 Human cDN	
2	2	3420.2	89.4	3436	6	AHH43509	Ahh14509 Human cDN	
3	3	3212	84.0	3243	9	ADC37268	ADC37268 Nuclear f	
4	4	2322.2	60.7	22893	6	ABK12810	ABK12810 Human tmm	
5	5	2319.8	60.6	5858	4	AAK80624	AAK80624 Human tmm	
6	6	2308.6	60.3	30676	6	ABK12811	ABK12811 Human tmm	
7	7	2306.2	60.3	5866	6	AAK80625	AAK80625 Human tmm	
8	8	2252.8	58.9	30625	6	ABK12808	ABK12808 Human tmm	
9	9	2252	58.9	5858	4	AAK80626	AAK80626 Human tmm	
10	10	1745.2	45.6	2246	9	ADC37266	ADC37266 Nuclear f	
11	11	1657.2	43.3	2207	9	ADC37454	ADC37454 Nuclear f	
12	12	1657.2	43.3	2207	9	ADC37264	ADC37264 Nuclear f	
13	13	995.8	26.0	45845	6	ABK12809	ABK12809 Human tmm	
14	14	838.6	21.9	49744	6	ABK12807	ABK12807 Human tmm	
15	15	592.2	15.5	628	4	AAH06784	Ahh06784 Human cDN	
C 16	16	562	14.7	573	4	AAI16850	Aai16850 Probe #67	
C 17	17	562	14.7	573	4	ABA60671	Aba60671 Human foe	
C 18	18	562	14.7	573	4	AAI40560	Aai40560 Probe #92	
C 19	19	562	14.7	573	4	ABA28765	Aba28765 Probe #72	
C 20	20	562	14.7	573	4	AAK34844	Aak34844 Human bon	
C 21	21	562	14.7	573	4	AAK08953	Aak08953 Human bra	
C 22	22	562	14.7	573	4	ABS34609	Abs34609 Human liv	
C 23	23	562	14.7	573	6	ABS09384	Abs09384 Human gen	

CC The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
 CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
 CC from 10-50 amino acids, an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells, a method for suppressing growth of a cancer cells by contacting
 CC the cells with the expression cassette (i.e. gene therapy), a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the expression of
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1, and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1
 XX
 SQ Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 U; 0 Other;

Query Match 100.0%; Score 3826; DB 6; Length 3826;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGCTGCGCTGACCGAAGCGGTGGCTGCTAAGCTCGCGGGGTAAAGGGTGGG 60
 DB 1 AGGCTGCGCTGACCGAAGCGGTGGCTGCTAAGCTCGCGGGGTAAAGGGTGGG 60
 QY 61 CCAGGGTTTGGGGCCGGGATCGGAGCTGAGCGGCGCGGACCCCTCTCTCTCTGCC 120
 DB 61 CCAGGGTTTGGGGCCGGGATCGGAGCTGAGCGGCGCGGACCCCTCTCTCTCTGCC 120
 QY 121 GGTTCAGAGCAATGTACGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 180
 DB 121 GGTTCAGAGCAATGTACGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 180
 QY 181 GGTTCAGAGCAATGTACGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
 DB 181 GGTTCAGAGCAATGTACGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
 QY 241 CCGGCTCGGGATCCCTTCTCCAGCTCTATCTCTCTAGGCTGGCCCGCCCTCTAGAA 300
 DB 241 CCGGCTCGGGATCCCTTCTCCAGCTCTATCTCTCTAGGCTGGCCCGCCCTCTAGAA 300
 QY 301 CTTCCCGCTCAGGATCTCCGCTCCTCAGCGCTCAGAGCTCTCTCCAGCGCCATGCC 360
 DB 301 CTTCCCGCTCAGGATCTCCGCTCCTCAGCGCTCAGAGCTCTCTCCAGCGCCATGCC 360
 QY 361 TTGAGTGGCCACTACCTCTAGACTGCTCCGGGCTGGGCTGGGCTGGGCTGGGCTGG 420
 DB 361 TTGAGTGGCCACTACCTCTAGACTGCTCCCGGCTGGGCTGGGCTGGGCTGGGCTGG 420
 QY 421 GCGACCCCTTCTCGCGTTTACCCCTCTCTCGGACAGCAGCCCTCTCTCTCGGTAGC 480

421 GCGACCCCTTCTCGCGTTTACCCCTCTCTCGGACAGCAGCCCTCTCTCTCTCGGTAGC 480
 QY 481 TCTACCCCTGCTGTCGGGCTGTCGTCGGGCGCCAGCCCTCTCTCTCTCGGTAGC 540
 DB 481 TCTACCCCTGCTGTCGGGCTGTCGTCGGGCGCCAGCCCTCTCTCTCTCGGTAGC 540
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 DB 541 GCGCGGCTCTCTCAGCGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
 QY 601 GCGATGCGGTGCGAGCTCTAAGGAGAGCTGTCGTGCTCTCTCTCTCTCTCTCTCTCT 660
 DB 601 GCGATGCGGTGCGAGCTCTAAGGAGAGCTGTCGTGCTCTCTCTCTCTCTCTCTCTCT 660
 QY 661 GACCGGTGAGCTGGGCTGCGAGCACTACTTCTGCGCGCGCTCTCTCTCTCTCTCTCT 720
 DB 661 GACCGGTGAGCTGGGCTGCGAGCACTACTTCTGCGCGCGCTCTCTCTCTCTCTCTCT 720
 QY 721 GTGCGGAGGAGGCGCGGCGCTGCGAGCTGTCGCGGCGCGGCGCGGCGCGGCGCGG 780
 DB 721 GTGCGGAGGAGGCGCGGCGCTGCGAGCTGTCGCGGCGCGGCGCGGCGCGGCGCGG 780
 QY 781 CCGCGGCTGGCGCCAGCTCAAGCTGCGCACTCTGTCGAGCGCTCAGCTCTCTCTCTCT 840
 DB 781 CCGCGGCTGGCGCCAGCTCAAGCTGCGCACTCTGTCGAGCGCTCAGCTCTCTCTCTCT 840
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 DB 841 CTGAGCGCATCTCTCAAGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
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 DB 901 AAGCTCTTCTGCTCTCAGCGACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
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 DB 961 CACGAGCGATCAGCTCAGCGCATCAGCGCGCTCTGAGCGAGGAGCTGAGCGAGGAG 1020
 QY 1021 AAGGACCACTTCAAGCGCGCGCTTCAAGCAGCGAGCGGGAACACACCGAGCGCTG 1080
 DB 1021 AAGGACCACTTCAAGCGCGCTTCAAGCAGCGAGCGGGAACACACCGAGCGCTG 1080
 QY 1081 CTTCAAGCGCAACTCGCGGAGACCAAGTCTTCCACAGAGCGCTGCGGACCATATCGGC 1140
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 QY 1141 GAGGCTTTCAGCGGCTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 DB 1141 GAGGCTTTCAGCGGCTGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 QY 1201 CTGAGGCGGACACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 DB 1201 CTGAGGCGGACACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
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 DB 1321 GACCGGCAACCTTCTCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1380
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 DB 1381 CATGAGACCAACTCTCATATGAAGCTTCCCGAGCTTCCAGTACAGGCGCCCTGTCAG 1440
 QY 1441 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACCTGCTGCTGCTGCTGCTGCTGCTG 1500
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 QY 1501 GACCGGCGCAGCGCCACCGAGCGCTGATCTCTCTGCGAGCAGCTGACCATGCTGCTGCT 1560

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Qy 1741 ATCCAGCCAGCGCGGCTTCTACTGATGCTGATGCAAGCCGCAAGGCGCATCCAG 1800
Db 1741 ATCCAGCCAGCGCGGCTTCTACTGATGCTGATGCAAGCCGCAAGGCGCATCCAG 1800
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Db 2041 AAGGAGAACCAACCTTCCTGGGACCACTGCCACTGCAAGAGCCCTGCCAGGAAGTAG 2100
Qy 2101 AAGACTGACTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAAGTTGTTACCCCTCC 2160
Db 2101 AAGACTGACTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAAGTTGTTACCCCTCC 2160
Qy 2161 AGCTCCAGTCTGTAAATGGAGTTGCATTCCTTACTTCTTAAACTCTCTTCCAGCATC 2220
Db 2161 AGCTCCAGTCTGTAAATGGAGTTGCATTCCTTACTTCTTAAACTCTCTTCCAGCATC 2220
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Db 2401 AGTTGGCAGCCGAAAGACACAGACCCCTTATGTGCCATGGCCTTAAGACTTACCCC 2460
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QY 3781 TGTATTAAATTTAAAGTTACAGAGTGTCAAAAAAATAAAAAA 3826
Db 3781 TGTATTAAATTTAAAGTTACAGAGTGTCAAAAAAATAAAAAA 3826

RESULT 2
AAH14509
ID AAH14509 standard; cDNA; 3436 BP.
XX AAH14509;
AC
XX
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:12036.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EPI074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX
XX 27-AUG-1999; 99JP-00300253.
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XX 11-JAN-2000; 2000JP-00118776.
XX
XX 02-MAY-2000; 2000JP-00183767.
XX
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX length cDNAs defined in the specification, and for the detection and/or
XX diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
XX
XX Claim 8; SEQ ID NO 12036; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 3'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in the
XX specification. The primer sets can be used in antisense therapy and in
XX gene therapy. The primers are useful for synthesizing polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
XX Sequence 3436 BP; 731 A; 1126 C; 901 G; 678 T; 0 U; 0 Other;
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Query Match 89.4%; Score 3420.2; DB 4; Length 3436;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 370 CCACTACCTCTAGACTGCCCTCCGGGCTGGGCTCCACGAGAGTCTCAGCGGGCAGCCCC 429
Db 1 CCACTACCTCTAGACTGCCCTCCGGGCTGGGCTCCACGAGAGTCTCAGCGGGCAGCCCC 60

QY 430 TTCTTGGCGTTACCTCTTCCGAGACAGACCCCTCCCTTCTCCGGTAGTCTTACCCC 489
Db 61 TTCTTGGCGTTACCTCTTCCGAGACAGACCCCTCCCTTCTCCGGTAGTCTTACCCC 120

QY 490 TGCTGTGGGGGCTCTGTCGCCGCCGAGCCCTCGGTGCTGCTCCGACAGAGCCCGGC 549
Db 121 TGCTGTGGGGGCTCTGTCGCCGCCGAGCCCTCGGTGCTGCTCCGACAGAGCCCGGC 180

QY 550 TTCTTCAAGCGCCCTTCCGAGACAGACCCCTCCCTTCTGCTGCTGCTGCGGCGCATGGCG 609
Db 181 TTCTTCAAGCGCCCTTCCGAGACAGACCCCTCCCTTCTGCTGCTGCTGCGGCGCATGGCG 240

QY 610 TGAAGCTCAAGAGAGAGTGTGTGCTTCAATCTGCTGAGCATCTACCAGAGCCCGGTG 669
Db 241 TGAAGCTCAAGAGAGAGTGTGTGCTTCAATCTGCTGAGCATCTACCAGAGCCCGGTG 300

QY 670 AGCTGGGCTCGAGAGCACTACTTCTGCGCGCTGTCATCAGGAGCACTGGGTGCGGCGAG 729
Db 301 AGCTGGGCTCGAGAGCACTACTTCTGCGCGCTGTCATCAGGAGCACTGGGTGCGGCGAG 360

QY 730 GAGCGCAGGCGCGCCGCGAGTGTGCGGCGGCGACGTTTGGCGGAGCCCGCGCTG 789
Db 361 GAGCGCAGGCGCGCCGCGAGTGTGCGGCGGCGACGTTTGGCGGAGCCCGCGCTG 420

QY 790 GCGCCAGCTCAAGCTGGGCGCAATCTGAGAGCGCTACAGTCTCTTCCGCTGAGAGCC 849
Db 421 GCGCCAGCTCAAGCTGGGCGCAATCTGAGAGCGCTACAGTCTCTTCCGCTGAGAGCC 480

QY 850 ATCTTCAAGCGCGCGCGCGCGAGCCCTTGCAGCGGCGACGACAAAGTCAAGTCTTTC 909
Db 481 ATCTTCAAGCGCGCGCGCGCGAGCCCTTGCAGCGGCGACGACAAAGTCAAGTCTTTC 540

QY 910 TGCCTCAGGACCGCGCGCTTCTGCTTCTTTCGAGAGCGCTGCACTGCAGAGAG 969
Db 541 TGCCTCAGGACCGCGCGCTTCTGCTTCTTTCGAGAGCGCTGCACTGCAGAGAG 600

QY 970 CATCAGTCAACGCGATCGACGAGCGCTTGCAGAGCTGCGAGGAGGAGTCAAGAGCCAA 1029
Db 601 CATCAGTCAACGCGATCGACGAGCGCTTGCAGAGCTGCGAGGAGGAGTCAAGAGCCAA 660

QY 1030 CTTTCAAGCGCGCGCGGAGACACACCGAAGCGCTGCAGTCTCTCAAGCGA 1089
Db 661 CTTTCAAGCGCGCGCGGAGACACACCGAAGCGCTGCAGTCTCTCAAGCGA 720

QY 1090 CAATGGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCTATTCGGGAGGCGCTTC 1149
Db 721 CAATGGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCTATTCGGGAGGCGCTTC 780

QY 1150 GAGCGGTGACACCGCTGCTGCGTGAAGCGGAGGCGCATGTAGAGAGCTGAGGCG 1209
Db 781 GAGCGGTGACACCGCTGCTGCGTGAAGCGGAGGCGCATGTAGAGAGCTGAGGCG 840

QY 1210 GACACGCGCGCGCGCTGACCGACATCGAGCAGAAAGTCCAGCGCTACAGCAGAGCTG 1269
Db 841 GACACGCGCGCGCGCTGACCGACATCGAGCAGAAAGTCCAGCGCTACAGCAGAGCTG 900

QY 1270 CGGAGGTTCAGAGGAGGAGCCAGATCTCGAGAGCGGCTGGCTGAACCGAGCGGAC 1329
Db 901 CGGAGGTTCAGAGGAGGAGCCAGATCTCGAGAGCGGCTGGCTGAACCGAGCGGAC 960

QY 1330 ACCTTCTGCTGGGTGGGCTCTCACTGTCGAGGCGGCTCAAGGGGAAAAATCCATGAGACC 1389
Db 961 ACCTTCTGCTGGGTGGGCTCTCACTGTCGAGGCGGCTCAAGGGGAAAAATCCATGAGACC 1020
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Db 3180 AGTCCTGGGCGCTAGATTCTGCACTTGGGCTCTGACACACACACATCCCAAGTAG 3239
 QY 3610 CCGAAGAGCTAAACACAGGGGGTCTTAAATATGGCTGGCCCGCCACCGGGGCTCCCT 3669
 Db 3240 CCGAAGAGCTAAACACAGGGGGTCTTAAATATGGCTGGCCCGCCACCGGGGCTCCCT 3299
 QY 3670 TGGGCAAAAGGAATGTGACGCTTACCCCAACCTTCAACTACAGAAATCTGGGCCACCC 3729
 Db 3300 TGGGCAAAAGGAATGTGACGCTTACCCCAACCTTCAACTACAGAAATCTGGGCCACCC 3359
 QY 3730 CAGCAGTATTTTATTTAAATATGTTGCCATTTATGAGTTATGATCAATTTGATTTAA 3789
 Db 3360 CAGCAGTATTTTATTTAAATATGTTGCCATTTATGAGTTATGATCAATTTGATTTAA 3419
 QY 3790 TTAAGTTACAGATGTC 3806
 Db 3420 TTAAGTTACAGATGTC 3436

RESULT 3
 ADC37268
 ID ADC37268 standard; DNA; 3243 BP.
 AC ADC37268;
 XX
 XX
 DT 18-DEC-2003 (first entry)
 XX
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 101.
 XX
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
 XX
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO2003048202-A2.
 XX
 XX
 PD 12-JUN-2003.
 XX
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 XX
 PA (ASAH) ASAMI KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI; 2003-505282/47.
 DR P-PSDB; ADC37269.
 XX
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 XX
 PS Claim 4; SEQ ID NO 101; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 XX
 SQ Sequence 3243 BP; 715 A; 1023 C; 863 G; 642 T; 0 U; 0 Other;

Query Match 84.0%; Score 3212; DB 9; Length 3243;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 3234; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 QY 571 CTTGGGGCCCCCTCTCTGCTGCCCCCTGGCCCATGCGCTGACGCTCAAGGACGAGCTG 630
 Db 10 CTTGGGGCCCCCTCTCTGCTGCCCCCTGGCCCATGCGCTGACGCTCAAGGACGAGCTG 69
 QY 631 CTGTGCTTCCATCTGCTGAGCATCTACAGACCCCGTGGCTGGGCTCGAGCACTAC 690
 Db 70 CTGTGCTTCCATCTGCTGAGCATCTACAGACCCCGTGGCTGGGCTCGAGCACTAC 129
 QY 691 TTCTGCCCGCTGCTGATCAACGAGCACTGGGTGGGAGGAGGCGAGGCGCCCGGAC 750
 Db 130 TTCTGCCCGCTGCTGATCAACGAGCACTGGGTGGGAGGAGGCGAGGCGCCCGGAC 189
 QY 751 TGGCCCGAGTGGCGGCGACGTTGGCCGAGCCCGCTGGGCGCCAGCCTCAAGCTGGCC 810
 Db 190 TGGCCCGAGTGGCGGCGACGTTGGCCGAGCCCGCTGGGCGCCAGCCTCAAGCTGGCC 249
 QY 811 AACATCGTGGAGCGCTACAGCTCTCTCCCGTGGACGCCATCTCTCAACGCGCGCGGCC 870
 Db 250 AACATCGTGGAGCGCTACAGCTCTCTCCCGTGGACGCCATCTCTCAACGCGCGCGGCC 309
 QY 871 GCGGACCTCGCAGGCGCAGCAAGGTCAAGCTCTTCTGCTCAGGACCGCGCGCTT 930
 Db 310 GCGGACCTCGCAGGCGCAGCAAGGTCAAGCTCTTCTGCTCAGGACCGCGCGCTT 369
 QY 931 CTCTGCTTCTCTGCGAGGAGCGCTGCACTGACGAGCAGCATCAGTCCACGCGCATCGAC 990
 Db 370 CTCTGCTTCTCTGCGAGGAGCGCTGCACTGACGAGCAGCATCAGTCCACGCGCATCGAC 429
 QY 991 GACGCTTTCGACGAGCTGCGAGGAGGCTGAAGGACCAACTTCAGGCGCTTCAAGACAGC 1050
 Db 430 GACGCTTTCGACGAGCTGCGAGGAGGCTGAAGGACCAACTTCAGGCGCTTCAAGACAGC 489
 QY 1051 GAGCGGAAACACACCGAAGCGCTGAGTCTGAAGGACCAACTTCAGGCGGAGCAACAGTCT 1110
 Db 490 GAGCGGAAACACACCGAAGCGCTGAGTCTGAAGGACCAACTTCAGGCGGAGCAACAGTCT 549
 QY 1111 TCACCAAGAGCGCTGCGGACCACTATCGGCGAGCGCTTCGAGCGGCTSCACCGGCTGCTG 1170
 Db 550 TCACCAAGAGCGCTGCGGACCACTATCGGCGAGCGCTTCGAGCGGCTGCAACGCGTGTG 609
 QY 1171 CGTGAAAGCGGAGGCGCTGAGAGGCTGAGGCGGACACGCGCGCGCACGCTGACC 1230
 Db 610 CGTGAAAGCGGAGGCGCTGAGAGGCTGAGGCGGACACGCGCGCGCACGCTGACC 669
 QY 1231 GACATCGAGCAGAAAGTTCAGCGCTACAGCAGAGCTGCGCAAGGTCAGGAGGAGCC 1290
 Db 670 GACATCGAGCAGAAAGTTCAGCGCTACAGCAGAGCTGCGCAAGGTCAGGAGGAGCC 729
 QY 1291 CAGATCTTCGAGGAGCGGCTGGCTGAAACCGGACACCTTCCTGGCTGGGCTGGGCC 1350
 Db 730 CAGATCTTCGAGGAGCGGCTGGCTGAAACCGGACACCTTCCTGGCTGGGCTGGGCC 789
 QY 1351 TCACTGTCCGAGCGGCTCAAGGGGAAAATCATGAGACCAACCTCAATATGAAGACTTC 1410
 Db 790 TCACTGTCCGAGCGGCTCAAGGGGAAAATCATGAGACCAACCTCAATATGAAGACTTC 849
 QY 1411 CCGACCTCCAGTACACAGGCGCCCTGAGTACACCATCTGGAAGTCCCTGTTCCAGGAC 1470
 Db 850 CCGACCTCCAGTACACAGGCGCCCTGAGTACACCATCTGGAAGTCCCTGTTCCAGGAC 909
 QY 1471 ATCCACCCAGTGGCAGCGCGCCCTAACCTTGACCGCGGACAGGCCACAGCGCTGATC 1530
 Db 910 ATCCACCCAGTGGCAGCGCGCCCTAACCTTGACCGCGGACAGGCCACAGCGCTGATC 969
 QY 1531 CTGTGCGAGCAGTGCACCAATTTGGCTTACGGCACTTGACCCACAGCCACTGAGGAC 1590
 Db 970 CTGTGCGAGCAGTGCACCAATTTGGCTTACGGCACTTGACCCACAGCCACTGAGGAC 1029
 QY 1591 TCGCCAAAGCGCTTCGATGTGAGGTGCGGTGCTGGGTTCTGAAGCCCTCAGTAGTGGC 1650
 Db 1030 TCGCCAAAGCGCTTCGATGTGAGGTGCGGTGCTGGGTTCTGAAGCCCTCAGTAGTGGC 1089

QY	1651	GTCCACTACTGGAGGTGGTGGCGGGAAGACCCAGTGGGTGATCGGGCTGGGCACAC	1710
Db	1090	GTCCACTACTGGAGGTGGTGGCGGGAAGACCCAGTGGGTGATCGGGCTGGGCACAC	1149
QY	1711	GAAGCCGCAAGCCGCAAGGCGAGCATCCAGATCCAGCCAGCCGCGCTTCTACTGCATC	1770
Db	1150	GAAGCCGCAAGCCGCAAGGCGAGCATCCAGATCCAGCCAGCCGCGCTTCTACTGCATC	1209
QY	1771	GTGATGCAAGTGGCAACGAGTACAGGCTGTGACGGAGCCCTGGAGCGGGCTTAAAGTC	1830
Db	1210	GTGATGCAAGTGGCAACGAGTACAGGCTGTGACGGAGCCCTGGAGCGGGCTTAAAGTC	1869
QY	1831	CGGCAAGCTTACAGAGTGGGTGTCTTCTGAGCTATGACCAAGGCTGTCTATCTTC	1890
Db	1270	CGGCAAGCTTACAGAGTGGGTGTCTTCTGAGCTATGACCAAGGCTGTCTATCTTC	1329
QY	1891	TACAATGCTGATGACATGCTGGCTCTACACCTTCCGCGAGAGTTCCTGGCAAGCTC	1950
Db	1330	TACAATGCTGATGACATGCTGGCTCTACACCTTCCGCGAGAGTTCCTGGCAAGCTC	1389
QY	1951	TGCTCTTACTTACGCTCGCCAGAGCGACGCAATGGCAAGAACGTTACGCGCTGGCG	2010
Db	1390	TGCTCTTACTTACGCTCGCCAGAGCGACGCAATGGCAAGAACGTTACGCGCTGGCG	1449
QY	2011	ATCAACACCGTCCGCATCTAGTCCAGGAGAGGACACACACCTTCTGGGACACTGC	2070
Db	1450	ATCAACACCGTCCGCATCTAGTCCAGGAGAGGACACACACCTTCTGGGACACTGC	1509
QY	2071	CACCTCAAGAGCCCTGCCAGGAAGATAGAACCTTGGACTCCAGCCACCGTGCCAC	2130
Db	1510	CACCTCAAGAGCCCTGCCAGG- AGATAGAACCTTGGACTCCAGCCACCGTGCCAC	1568
QY	2131	TGGAGACCTCAGCCAGTTGTTTACCTTCAGCTCCAGCTCTGTAATAATGGAGTTGCAT	2190
Db	1569	TGGAGACCTCAGCCAGTTGTTTACCTTCAGCTCCAGCTCTGTAATAATGGAGTTGCAT	1628
QY	2191	TCCTTACTTCTTAACTCTTCCAGATCGATGTTCTGTAGTCTGACTTGATAGGA	2250
Db	1629	TCCCTACTTCTTAACTCTTCCAGATCGATGTTCTGTAGTCTGACTTGATAGGA	1688
QY	2251	TACAGTTTGTATCCAAAGGATGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCT	2310
Db	1689	TACAGTTTGTATCCAAAGGATGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCT	1748
QY	2311	GATCCCATCTTCTCAGGGGAGGGACCTACCTTCAGTGTCTCCCTCAGGCCAGCCCT	2370
Db	1749	CATCCCATCTTCTCAGGGGAGGGACCTACCTTCAGTGTCTCCCTCAGGCCAGCCCT	1808
QY	2371	GACCTCAGGAAGTGTACAGAGCATGGCCAGTAGTTGGCAGCCGGAAGACACACAGCCC	2430
Db	1809	GACCTCAGGAAGTGTACAGAGCATGGCCAGTAGTTGGCAGCCGGAAGACACACAGCC	1867
QY	2431	TCTTATGTCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCT	2490
Db	1868	TCTTATGTCCCATGGCTTAAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCT	1927
QY	2491	TGACCCAGTCCACAGTGTACAGTAGTACTTGTCTTAGTGTCTCCTGAGAGCCAC	2550
Db	1928	TGACCCAGTCCACAGTGTACAGTAGTACTTGTCTTAGTGTCTCCTGAGAGCCAC	1987
QY	2551	CTCTCTGCGACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTCCCACTGATCTGCTG	2610
Db	1988	CTCTCTGCGACCCCCACACCAAGAACTATATGTTCTTCTTCTTCTCCCACTGATCTGCTG	2047
QY	2611	GTCAAGTATGATCTGTGGCTGTGGAGGCACTTGGTAGTTGAGTCCACATATAGT	2670
Db	2048	GTCAAGTATGATCTGTGGCTGTGGAGGCACTTGGTAGTTGAGTCCACATATAGT	2107
QY	2671	CATGTGCCACCACTTCTGCCACAGGCCGAGGACAGGGTGAGGGTATACCAAGCT	2730
Db	2108	CATGTGCCACCACTTCTGCCACAGGCCGAGGACAGGGTGAGGGTATACCAAGCT	2167

QY	2731	GATGCAGAGCCCATTTAGCCTTAAAGCAACTGCGAGGACAAGCCTCCCTGATGATCGAGGT	2790
Db	2168	GATGCAGAGCCCATTTAGCCTTAAAGCAACTGCGAGGACAAGCCTCCCTGATGATCGAGGT	2227
QY	2791	CCCACCTAGTCTCTGAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGGCTCTGTGACCTGC	2850
Db	2228	CCCACCTAGTCTCTGAACAAGAGTCCAGCCAAACCTCTTTCAGCCAGGCTCTGTGACCTGC	2287
QY	2851	TAGGTCGAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACTGGAGGG	2910
Db	2288	TAGGTCGAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACTGGAGGG	2347
QY	2911	CTGTCGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGGATCTGCTGAGAA	2970
Db	2348	CTGTCGGCTAGACCCCTTGTTCAGACTTGGCATCTATCTCAGTTAGGATCTGCTGAGAA	2407
QY	2971	AACAAGAGCCACTTGTAGCTGGTTTAAATTAGACAAGATTTACTACTGCGCCCTGGTGG	3030
Db	2408	AACAAGAGCCACTTGTAGCTGGTTTAAATTAGACAAGATTTACTACTGCGCCCTGGTGG	2467
QY	3031	CTTGCAAAATTTGTGAAGAGCTGGAGAACAGACTCTCTGTAATTTCCAGGAACTCCCA	3090
Db	2468	CTTGCAAAATTTGTGAAGAGCTGGAGAACAGACTCTCTGTAATTTCCAGGAACTCCCA	2527
QY	3091	GGCCAGATTCATCTGTCTGTGTGACCAAGAAAGCTGCCCCATCTCGAGGAAGCCAC	3150
Db	2528	GGCCAGATTCATCTGTCTGTGTGACCAAGAAAGCTGCCCCATCTCGAGGAAGCCAC	2587
QY	3151	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCA	3210
Db	2588	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCA	2647
QY	3211	ATAGATGCTCAGGCTGCGCTCTCCCACTTCTCAGTTCTCAGTTCCCAAACTTAAATTTTA	3270
Db	2648	ATAGATGCTCAGGCTGCGCTCTCCCACTTCTCAGTTCTCAGTTCCCAAACTTAAATTTTA	2707
QY	3271	CAAGAGATTTCTGTTGGGGAACTTAAAGTCCAGATCCAGAACCTTGGCTGCAAGGGAGTCT	3330
Db	2708	CAAGAGATTTCTGTTGGGGAACTTAAAGTCCAGATCCAGAACCTTGGCTGCAAGGGAGTCT	2767
QY	3331	GGAAATGTCAATTCCTTAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCCACCTCGGTTT	3390
Db	2768	GGAAATGTCAATTCCTTAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCCACCTCGGTTT	2827
QY	3391	TTCTGCCACAGCATCAATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGGTT	3450
Db	2828	TTCTGCCACAGCATCAATCGTGAAGAACTCGGGAGAGGTGGAGTCCACATCTAGGGTT	2887
QY	3451	GTCTTCCCTTGGCTCTATCCCTGCCAGAGTGGAACTCGAGAGTGGGGTGCAGGA	3510
Db	2888	GTCTTCCCTTGGCTCTATCCCTGCCAGAGTGGAACTCGAGAGTGGGGTGCAGGA	2947
QY	3511	CTGAGCTAAATGTCTCCCGGCTTGACTTTTCTTCTAGTCTCTGGGCTAGATTCTG	3570
Db	2948	CTGAGCTAAATGTCTCCCGGCTTGACTTTTCTTCTAGTCTCTGGGCTAGATTCTG	3007
QY	3571	CACTTGGGGTCTCTGACACACACACATCCCAAAGTAGCCGGAAGAGCTAAACAGGG	3630
Db	3008	CACITGGGGTCTCTGACACACACACATCCCAAAGTAGCCGGAAGAGCTAAACAGGG	3067
QY	3631	GGTTCCTTAAATGGTGGCCCCCGCACCGGGCTCCCTTGGGCAAAAGGAATTTGTACG	3690
Db	3068	GGTTCCTTAAATGGTGGCCCCCGCACCGGGCTCCCTTGGGCAAAAGGAATTTGTACG	3127
QY	3691	CCTACCCCAACCTTCAACTACAGAACTTGGGCCACCCCAAGCACTATTTTATTTAAA	3750
Db	3128	CCTACCCCAACCTTCAACTACAGAACTTGGGCCACCCCAAGCACTATTTTATTTAAA	3187
QY	3751	TGTTGCCCATTTTATGAGTTATGATCAATTTGATTAATTAAGTTACAGATGC	3806
Db	3188	TGTTGCCCATTTTATGAGTTATGATCAATTTGATTAATTAAGTTACAGATGC	3243

RESULT 4

ABK12810
ID ABK12810 standard; DNA; 22893 BP.

XX AC ABK12810;

XX DT 18-JUN-2002 (first entry)

XX DE Human tumour suppressor CAR-1, BAC clone RP11-150F21 3' sequence.

XX KW Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteriophage chromosome; chromosome 1p31-1p36.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT misc_feature 5820

FT FT /*tag= a
FT /note= "Nucleotides 5821-6360 of the present sequence as
FT reproduced in the specification are illegible or missing,
FT nucleotide 5821 of the present sequence corresponds to
FT nucleotide 6361 of sequence as printed in the
FT specification"

XX PN WO200212285-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US025269.

XX PR 10-AUG-2000; 2000US-0225033P.

XX PR 23-AUG-2000; 2000US-0227560P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Killary A, Chandler D, Lott S;

XX WPI; 2002-269089/31.

XX PT New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.

XX PS Disclosure; Page 170-176; 185pp; English.

XX CC The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumor suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,

CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene

XX SQ Sequence 22893 BP; 5720 A; 5989 C; 5664 G; 5415 T; 0 U; 105 Other;

Query Match 60.7%; Score 2322.2; DB 6; Length 22893;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2350; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

Qy	1429	GGCCCCCTTGAGTACACCATCTCGAAGTCCCTGTTCCAGACATCCACCAGTGCACGCC	1488
Db	11940	GGTCCACAGCCTTCTCCCACTCATCTTCTCTCCCTCTCCAAACCCACACAGTGCCAGCC	11999
Qy	1489	GCCTTAACCTTGACCCGGGCACAGCCACAGCGCTGATCCTGTCGACGACTGCACCC	1548
Db	12000	GCCTTAACCTTGACCCGGGCACAGCCACAGCGCTGATCCTGTCGACGACTGCACCC	12059
Qy	1549	ATTGTGGCTTTACGGCAACTTGCACCCACAGCCACTGCAGGACTGCACAAAGCGTTCCGAT	1608
Db	12060	ATTGTGGCTTTACGGCAACTTGCACCCACAGCCACTGCAGGACTGCACAAAGCGTTCCGAT	12119
Qy	1609	GTGAGGTGTCGGTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTCTGGAGGTG	1668
Db	12120	GTGAGGTGTCGGTCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTACTCTGGAGGTG	12179
Qy	1669	GTGTGGCGGAGAGAACCCAGTGGGTGATCGGGTGGCACACAGCGGCGAAGCGCGAAG	1728
Db	12180	GTGTGGCGGAGAGAACCCAGTGGGTGATCGGGTGGCACACAGCGGCGAAGCGCGAAG	12239
Qy	1729	GGCAGATCCAGATCCAGCCCGCGGTTCTTACTGTCATCGTGTGATGCAGATGGCAAC	1788
Db	12240	GGCAGATCCAGATCCAGCCCGCGGTTCTTACTGTCATCGTGTGATGCAGATGGCAAC	12299
Qy	1789	CAGTACAGCCCTGCACGGAGCCCTGACCGGGCTTAACTGTCGGGCAAGCTTGACAAAG	1848
Db	12300	CAGTACAGCCCTGCACGGAGCCCTGACCGGGCTTAACTGTCGGGCAAGCTTGACAAAG	12359
Qy	1849	GTGGGTCTCTTCTGGACTATGACCAAGGTTGCTCATCTTCTACAAATGCTGATGACATG	1908
Db	12360	GTGGGTCTCTTCTGGACTATGACCAAGGTTGCTCATCTTCTACAAATGCTGATGACATG	12419
Qy	1909	TCTTGGCTCTACACCTTCCCGAGAAAGTTCCTTGGCAAGCTTGTCTTTACTTTCAGGCCT	1968
Db	12420	TCTTGGCTCTACACCTTCCCGAGAAAGTTCCTTGGCAAGCTTGTCTTTACTTTCAGGCCT	12479
Qy	1969	GGCCAGAGCCACGCCAATGCAAGAAAGTTTACGCCCTGGGATCAACACCGTCCGCATC	2028
Db	12480	GGCCAGAGCCACGCCAATGCAAGAAAGTTTACGCCCTGGGATCAACACCGTCCGCATC	12539
Qy	2029	TAGTCCAGGAGAGAGAGACCAACAACTCTCTGGGACCACTGCCACCTGCAAGAGCCCTGC	2088
Db	12540	TAGTCCAGGAGAGAGAGACCAACAACTCTCTGGGACCACTGCCACCTGCAAGAGCCCTGC	12599
Qy	2089	CCAGAAAGATAGAAAGACTCGACTCCAGCCCAACCGTGGGCCACTGGAGACCTCAGGCCAGT	2148
Db	12600	CCAGG-AGATAGAGAGACTCGACTCCAGCCCAACCGTGGGCCACTGGAGACCTCAGGCCAGT	12658
Qy	2149	TGTTTACCTCCAGCCTCCAGTCTGTAAATGGAGGTTGCAATTCCTTACTTCTTAAACTC	2208
Db	12659	TGTTTACCTCCAGCCTCCAGTCTGTAAATGGAGGTTGCAATTCCTTACTTCTTAAACTC	12718

QY 2209 TCTTCAGCATCGATGTTCTGTAGTCTGACCTTGATAGGGATACAGCTTTTGATCCAAGG 2268
DB |||||
DB 12719 TCTTCAGCATCGATGTTCTGTAGTCTGACCTTGATAGGGATACAGCTTTTGATCCAAGG 12778
QY 2269 ATGTGACATGGCTTCTCCTCAGGCAACCCCTGCCAACCCCTCATCCCCATCTTCTCAGG 2328
DB |||||
DB 12779 ATGTGACATGGCTTCTCCTCAGGCAACCCCTGCCAACCCCTCATCCCCATCTTCTCAGG 12838
QY 2329 GGCAGGAGCTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGAG 2388
DB |||||
DB 12839 GGCAGGAGCTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGAG 12898
QY 2389 AGCATGGCCAGTAGTGTGGCAGCCCGAAGACACACAGCAGCACCCTCTTATGTCTCCATGGCT 2448
DB |||||
DB 12899 AGCATGGCCAGTAGTGTGGCAGCCCGAAGACACACAGCAGCACCCTCTTATGTCTCCATGGCT 12958
QY 2449 AAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTG 2508
DB |||||
DB 12959 AAGACTTACCCCTGACCAAGCTAGTGTGGGCCATTTACCCCTTGACCCAGTCCACAGTG 13018
QY 2509 GTCAGAGTGTAGTACCTGTCTTAGGTTGCTCAGAGCCCAACCTCTCCTGCCACCCCCAC 2568
DB |||||
DB 13019 GTCAGAGTGTAGTACCTGTCTTAGGTTGCTCAGAGCCCAACCTCTCCTGCCACCCCCAC 13078
QY 2569 ACCAAGAACTATATGTTTCTACTTCTCCACTGATCTGCTGCTCAGTGAATGATGCTGTG 2628
DB |||||
DB 13079 ACCAAGAACTATATGTTTCTACTTCTCCACTGATCTGCTGCTCAGTGAATGATGCTGTG 13138
QY 2629 GCCTGTGGAAGCACTGCTAGTGTAGTGTCCACATTTAGTGTGTCACCACTTCC 2688
DB |||||
DB 13139 GCCTGTGGAAGCACTGCTAGTGTAGTGTCCACATTTAGTGTGTCACCACTTCC 13198
QY 2689 TGCCACAGGCGGAGGACAGGTCAGGGTATACCAAGCTGATGTCAGAGCCCATTAGC 2748
DB |||||
DB 13199 TGCCACAGGCGGAGGACAGGTCAGGGTATACCAAGCTGATGTCAGAGCCCATTAGC 13258
QY 2749 CTAAAGCAACTGACGAGCAAGCTCCCTGGATGATCGAGGTCCCGAGTAGTCTGGAACA 2808
DB |||||
DB 13259 CTAAAGCAACTGACGAGCAAGCTCCCTGGATGATCGAGGTCCCGAGTAGTCTGGAACA 13318
QY 2809 AGAGTCCAGCCAAACCTCTTACGACAGGCTCTGTGACCTGTGAGGTCGAGGAGGCTTC 2868
DB |||||
DB 13319 AGAGTCCAGCCAAACCTCTTACGACAGGCTCTGTGACCTGTGAGGTCGAGGAGGCTTC 13378
QY 2869 CAGAGCAGTGTCTTAATTAGGACCCAGCACTGGAGGGCTGTGGCTAGACCCCTT 2928
DB |||||
DB 13379 CAGAGCAGTGTCTTAATTAGGACCCAGCACTGGAGGGCTGTGGCTAGACCCCTT 13438
QY 2929 GTCAGACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAACAAAGAGCCACTTGTAG 2988
DB |||||
DB 13439 GTCAGACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAACAAAGAGCCACTTGTAG 13498
QY 2989 CTGGTTTAAATAGACAAGATTTACTACCTGCCCCCTGGTGGCTTGCAAAATTTGTGGAA 3048
DB |||||
DB 13499 CTGGTTTAAATAGACAAGATTTACTACCTGCCCCCTGGTGGCTTGCAAAATTTGTGGAA 13558
QY 3049 GAGCTGGAGAGACAGACTCTGTAATTTCCAGGAACCTCCAGCCAGCTTTCATCATGT 3108
DB |||||
DB 13559 GAGCTGGAGAGACAGACTCTGTAATTTCCAGGAACCTCCAGCCAGCTTTCATCATGT 13618
QY 3109 CTGTTGTGACAGGAAGCTGCCCCCATCTGAGGAAGCACTATGCCAGAAAAGCTGTG 3168
DB |||||
DB 13619 CTGTTGTGACAGGAAGCTGCCCCCATCTGAGGAAGCACTATGCCAGAAAAGCTGTG 13678
QY 3169 ACTGCAGAACTAGGCTCCCTCTGCCCAGCGTCCGTCGCGCAAGCAATAGATGTCTCTGAGGCT 3228
DB |||||
DB 13679 ACTGCAGAACTAGGCTCCCTCTGCCCAGCGTCCGTCGCGCAAGCAATAGATGTCTCTGAGGCT 13738
QY 3229 GCCCTCTCCCACTTCACTCAGTTCCTCAAACTAAATTTTACAGAGATTTCTGTTGGG 3288
DB |||||
DB 13739 GCCCTCTCCCACTTCACTCAGTTCCTCAAACTAAATTTTACAGAGATTTCTGTTGGG 13798
QY 3289 GGAACCTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAATGTCATTTCCT 3348

DB 13799 GGAACCTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAATGTCATTTCCT 13858
QY 3349 AGAAGAACTTAGGTGGGTGGAGCAAGCCACCTGCGTTTTTCTGCCACAGCATCCAA 3408
DB |||||
DB 13859 AGAAGAACTTAGGTGGGTGGAGCAAGCCACCTGCGTTTTTCTGCCACAGCATCCAA 13918
QY 3409 TCGTCAAGAACTCGGAGAGGGTGSAGTCCACATCTAGGGTTGTCTGCCCTTGGCTCT 3468
DB |||||
DB 13919 TCGTCAAGAACTCGGAGAGGGTGSAGTCCACATCTAGGGTTGTCTGCCCTTGGCTCT 13978
QY 3469 ATCCCTGCCCAGAGGTGGGAACCTGAGGAGTGGGCTGCAAGACTGAGCTAAATGTCTCC 3528
DB |||||
DB 13979 ATCCCTGCCCAGAGGTGGGAACCTGAGGAGTGGGCTGCAAGACTGAGCTAAATGTCTCC 14038
QY 3529 CCGGCTTGTGACTTTTCTTAGTCTCTGGGCTTAGATTCTGCACTTGGGGTCTCTGACA 3588
DB |||||
DB 14039 CCGGCTTGTGACTTTTCTTAGTCTCTGGGCTTAGATTCTGCACTTGGGGTCTCTGACA 14098
QY 3589 CACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGC 3648
DB |||||
DB 14099 CACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGC 14158
QY 3649 CCCCCCACCCGGGCTCCCTTGGGCAAAAGGAATTTGTGAGCCCTACCCCAACCTTCAA 3708
DB |||||
DB 14159 CCCCCCACCCGGGCTCCCTTGGGCAAAAGGAATTTGTGAGCCCTACCCCAACCTTCAA 14218
QY 3709 CTACAGAACTTGGGCCACCCAGCAGTATTTTAAATTTTAAATTTTAAATTTTATGAG 3768
DB |||||
DB 14219 CTACAGAACTTGGGCCACCCAGCAGTATTTTAAATTTTAAATTTTAAATTTTATGAG 14278
QY 3769 TTATGATCAATTTGTATTAAATTTAAATTTAAATTTAAATTTTAAATTTTAAATTTGATCA 3807
DB |||||
DB 14279 TTATGATCAATTTGTATTAAATTTAAATTTAAATTTAAATTTTAAATTTTAAATTTGATCA 14317

RESULT 5
AAK80624
ID AAK80624 standard; DNA; 5858 BP.
XX
AC AAK80624;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35436.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.

CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 5858 BP; 1455 A; 1579 C; 1490 G; 1334 T; 0 U; 0 Other;
Query Match 60.6%; Score 2319.8; DB 4; Length 5858;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2332; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1473 CCACCCAGTGCACAGCGCCCTAACCCCTGACCCGGGACAGCCCAAGCGGCTGATCCT 1532
DB 1 CCCACAGTGCACAGCGCCCTAACCCCTGACCCGGGACAGCCCAAGCGGCTGATCCT 60
QY 1533 GTCCGAGCACTGCACCAATTTGTGGCTTACGGCACTTGCACCCACAGCCCACTCAGGACTC 1592
DB 61 GTCCGAGCACTGCACCAATTTGTGGCTTACGGCACTTGCACCCACAGCCCACTCAGGACTC 120
QY 1593 GCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGTTCCTGAAGCCCTTCAGTAGTGGGT 1652
DB 121 GCCAAAGCGCTTCGATGTGGAGGTGTCGGTGTGGTTCCTGAAGCCCTTCAGTAGTGGGT 180
QY 1653 CCACCTACTGGGAGGTGGTGGCGGAGAGAACCCAGTGGGTGATCGGCTGGCACAGA 1712
DB 181 CCACCTACTGGGAGGTGGTGGCGGAGAGAACCCAGTGGGTGATCGGCTGGCACAGA 240
QY 1713 AGCCGAGCGGAGGGGAGCATTCAGATCCAGCCAGCCGGGGTTCCTACTGCATCGT 1772
DB 241 AGCCGAGCGGAGGGGAGCATTCAGATCCAGCCAGCCGGGGTTCCTACTGCATCGT 300
QY 1773 GATGCACGATGCAACCACTGACAGGCTTCAGCGGCTTCGAGCGGCTTAAAGCTCG 1832
DB 301 GATGCACGATGCAACCACTGACAGGCTTCGAGCGGCTTCGAGCGGCTTAAAGCTCG 360
QY 1833 GGCAAGCTTGAAGAAGTGGGTGTCTTCTGGACTATGACCAAGGCTTCTCATCTTCTA 1892
DB 361 GGCAAGCTTGAAGAAGTGGGTGTCTTCTGGACTATGACCAAGGCTTCTCATCTTCTA 420
QY 1893 CAATGCTGATGATGTCTGCTGCTACACCTTCGCGAGAAGTTCCCTGGCAAGCTCTG 1952
DB 421 CAATGCTGATGATGTCTGCTGCTACACCTTCGCGAGAAGTTCCCTGGCAAGCTCTG 480
QY 1953 CTCTTACTTTCAGCCCTGGCCAGAGCCACGCCCAATGCAAGAACGTTTCAGCCGCTGGGAT 2012
DB 481 CTCTTACTTTCAGCCCTGGCCAGAGCCACGCCCAATGCAAGAACGTTTCAGCCGCTGGGAT 540
QY 2013 CAACACCGTCCGCACTTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTGCCA 2072
DB 541 CAACACCGTCCGCACTTAGTCCAGGAGAGGAGACCAACCTCTCTGGGACCACTGCCA 600
QY 2073 CCGTGAAGCCCTGCCAGGAGATAGAGACCTGGACTCCAGCCACCGTGGCCACTG 2132
DB 601 CCGTGAAGCCCTGCCAGGAGATAGAGACCTGGACTCCAGCCACCGTGGCCACTG 659
QY 2133 GAGACTCAGGCGAGTGTGTTTACCCCTCAGGCTCCAGTCTGTAAATGAGGTTGCATTC 2192
DB 660 GAGACTCAGGCGAGTGTGTTTACCCCTCAGGCTCCAGTCTGTAAATGAGGTTGCATTC 719
QY 2193 CTTACTTCTAACTCTCTTCAGCATGATGTTCTGTAGCTCTGACCTTGATAGGATA 2252
DB 720 CTTACTTCTAACTCTCTTCAGCATGATGTTCTGTAGCTCTGACCTTGATAGGATA 779
QY 2253 CAGCTTTGATCCAGGATGTGACATGGCTTCTCCTCAGGGCAACCCCTGCCAACCCCTCA 2312
DB 780 CAGCTTTGATCCAGGATGTGACATGGCTTCTCCTCAGGGCAACCCCTGCCAACCCCTCA 839
QY 2313 TCCCATCTTCTCAGGGGAGGGGACTACTCTTCCAGTGTCTCCTCAGCCAGCCCTGCA 2372
DB 840 TCCCATCTTCTCAGGGGAGGGGACTACTCTTCCAGTGTCTCCTCAGCCAGCCCTGCA 899
QY 2373 CTTAGGAAGTGTACAGCATGSCCAGTAGTGTGGAGCCGAGCAAGACACACAGCACCTTC 2432
DB 900 CTTAGGAAGTGTACAGCATGSCCAGTAGTGTGGAGCCGAGCAAGACACACAGCACCTTC 959

QY 2433 TTATGTCCCATGGCCCTAAGACTTACCCCTGACCAAGCTAGTGTATGGGCCATTTACCCCTTG 2492
DB 960 TTATGTCCCATGGCCCTAAGACTTACCCCTGACCAAGCTAGTGTATGGGCCATTTACCCCTTG 1019
QY 2493 ACCCCAGTCCACAGTGTGCACAGGTAGTACCTGGTTCCTAGGTTGCTCTGAGAGCCAACT 2552
DB 1020 ACCCCAGTCCACAGTGTGCACAGGTAGTACCTGGTTCCTAGGTTGCTCTGAGAGCCAACT 1079
QY 2553 CTCCTGCCACCCCCACACCAAGAACTATATGTTTCTTACTTCTCCCACTGATCTGCTGT 2612
DB 1080 CTCCTGCCACCCCCACACCAAGAACTATATGTTTCTTACTTCTCCCACTGATCTGCTGT 1139
QY 2613 CAGTGTATGATGTGTGGCTGTGGAGGCACTGTGTAGTGTGATCCACATATATGCTA 2672
DB 1140 CAGTGTATGATGTGTGGCTGTGGAGGCACTGTGTAGTGTGATCCACATATATGCTA 1199
QY 2673 TGTGCCACCACTTCTGTCGCCACAGGCCGAGGGAAGGTTAGGGGTATATCCCAAAGCTCA 2732
DB 1200 TGTGCCACCACTTCTGTCGCCACAGGCCGAGGGAAGGTTAGGGGTATATCCCAAAGCTCA 1259
QY 2733 TGCAGAGCCCACTTAGCCCTAAAAGCACTGCAGGAACAAGCTCCCTGGATGATCGAGTCC 2792
DB 1260 TGCAGAGCCCACTTAGCCCTAAAAGCACTGCAGGAACAAGCTCCCTGGATGATCGAGTCC 1319
QY 2793 CCAGTAGCTCTGAAACAAGAGTCCAGGCAACCTCTTCCAGCAGGCTCTGTGACCTGCTA 2852
DB 1320 CCAGTAGCTCTGAAACAAGAGTCCAGGCAACCTCTTCCAGCAGGCTCTGTGACCTGCTA 1379
QY 2853 GGGTGCAGGAGCTTCCAGAGCAGTGTGTAAATTTAGGACCAAGCACTGGGAGGGCT 2912
DB 1380 GGGTGCAGGAGCTTCCAGAGCAGTGTGTAAATTTAGGACCAAGCACTGGGAGGGCT 1439
QY 2913 GTTGGCTAGACCCCTTGTGATCTTGGGCACTATCTCAGTTAGGATCTGTGTCAGAAAA 2972
DB 1440 GTTGGCTAGACCCCTTGTGATCTTGGGCACTATCTCAGTTAGGATCTGTGTCAGAAAA 1499
QY 2973 CAAAGCCACTTGTAGCTGGTAAATTTAGCAAGGATTTACTACCTGGCCCTGGTGGCT 3032
DB 1500 CAAAGCCACTTGTAGCTGGTAAATTTAGCAAGGATTTACTACCTGGCCCTGGTGGCT 1559
QY 3033 TGCAAAATTTGTGGAGAGCTGGGAAAGCAGACTCTGCTGTAATTTCCAGGAATCTCCAGC 3092
DB 1560 TGCAAAATTTGTGGAGAGCTGGGAAAGCAGACTCTGCTGTAATTTCCAGGAATCTCCAGC 1619
QY 3093 GCCAGATTCACTCATGTCTGTTGTGACAGGAAAGCTGCCCCCATCTGCAAGGAGGCACTA 3152
DB 1620 GCCAGATTCACTCATGTCTGTTGTGACAGGAAAGCTGCCCCCATCTGCAAGGAGGCACTA 1679
QY 3153 TGCCAGAAAGCTGCTGACTGCAAGAACTAGGCTCCCTCTGCCAGGTCGGTGCAGGCAAT 3212
DB 1680 TGCCAGAAAGCTGCTGACTGCAAGAACTAGGCTCCCTCTGCCAGGTCGGTGCAGGCAAT 1739
QY 3213 AGATGCTCCTGAGGCTGCCCCCTCTCCCACTTCACTCAGTTCCCAATCTAAATTTTACA 3272
DB 1740 AGATGCTCCTGAGGCTGCCCCCTCTCCCACTTCACTCAGTTCCCAATCTAAATTTTACA 1799
QY 3273 AGAGATTCTGTTGGGGGAACTTAAGTCAAGTCCAGAACCTTGGCTGCAAGGAGTCTGG 3332
DB 1800 AGAGATTCTGTTGGGGGAACTTAAGTCAAGTCCAGAACCTTGGCTGCAAGGAGTCTGG 1859
QY 3333 GAAATGTCAATTTCCCTAGAAGGAGTTAGGGTGGGAGCAAGCCCACTGCGTTTTT 3392
DB 1860 GAAATGTCAATTTCCCTAGAAGGAGTTAGGGTGGGAGCAAGCCCACTGCGTTTTT 1919
QY 3393 CTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGTTGT 3452
DB 1920 CTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGGGTGGAGTCCACATCTAGGTTGT 1979
QY 3453 CTTGCCCTTGGCTCTATCCCTGCCCCAGAGTGGGAACTGGAAGGAGTGGGCTGCAAGACT 3512
DB 1980 CTTGCCCTTGGCTCTATCCCTGCCCCAGAGGTGGGAACTGGAAGGAGTGGGCTGCAAGACT 2039

QY 3513 GAGCTAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGGCTTAGATTCTGCA 3572
Db |||||
QY 2040 GAGCTAAATGTCTCCCGGCTTGAATTTCTTTCTAGTCTGGGGCTTAGATTCTGCA 2099
Db |||||
QY 3573 CTTGGGCTCTTGACACACACACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGG 3632
Db CTTGGGCTCTTGACACACACACACACATCCCAAGTAGCCGGAAGAGCTAAACACAGGGGG 2159
QY 3633 TTCTTAAATGGTGGCCCGGCGCACCGGGCTCCCTTTGGGCAAAAGAAATGTCAGCCC 3692
Db TTCTTAAATGGTGGCCCGGCGCACCGGGCTCCCTTTGGGCAAAAGAAATGTCAGCCC 2219
QY 3693 TACCCAAACCTTCAACTACAGATCTGGGCCACCCAGCAGTATTTTATTAAATG 3752
Db TACCCAAACCTTCAACTACAGATCTGGGCCACCCAGCAGTATTTTATTAAATG 2279
QY 3753 TTGCCCAATTTATGAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTCA 3807
Db TTGCCCAATTTATGAGTTATGATCAATTTGTTATTAATTTAAAGTTACAGATGTCA 2334

RESULT 6
ABK12811
ID ABK12811 standard; DNA; 30676 BP.
AC ABK12811;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor CAR-1, BAC clone RP11-131M11.
XX
KW Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteriophage artificial chromosome; chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX
FN WO200212285-A2.
PN 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025269.
XX
XX 10-AUG-2000; 2000US-0225033P.
PR 23-AUG-2000; 2000US-0227560P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Killary A, Chandler D, Lott S;
XX
XX WPI; 2002-269088/31.
DR
XX
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Disclosure; Page 176-185; 185pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating

CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
XX

SQ Sequence 30676 BP; 7591 A; 7621 C; 7888 G; 6944 T; 0 U; 632 Other;
Query Match 60.3%; Score 2308.6; DB 6; Length 30676;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2348; Conservative 0; Mismatches 29; Indels 2; Gaps 2;
QY 1429 GGCCCCCTGCGAGTACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCAGTCCGAGCC 1488
Db 23371 GGTTCCACAGCCTTCTCCCACTCATCTTCTCTCCCTCTCCCAACCCCAAGTCCGAGCC 23430
QY 1489 GCCTTAACCTGGACCCGGGCGGACAGCCACAGCGCTGATCTCTGGAGCATGTCGACC 1548
Db 23431 GCCTTAACCTGGACCCGGGCGGACAGCCACAGCGCTGATCTCTGGAGCATGTCGACC 23490
QY 1549 ATTGTGCTTTACGGCAACTTGCACCCACAGCCACTGCGAGCATGCGCAAGCGTTCGAT 1608
Db 23491 ATTGTGCTTTACGGCAACTTGCACCCACAGCCACTGCGAGCATGCGCAAGCGTTCGAT 23550
QY 1609 GTGAGGTGTCGGTGTCTGGGTCTGGAAGCCTTCAGTAGTGGCGTCCACTACTGGAGGTG 1668
Db 23551 GTGAGGTGTCGGTGTCTGGGTCTGGAAGCCTTCAGTAGTGGCGTCCACTACTGGAGGTG 23610
QY 1669 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGCTGGCACACAGAGCCGCAAGCCGCAAG 1728
Db 23611 GTGTGGCGGAGAAAGACCCAGTGGGTGATCGGCTGGCACACAGAGCCGCAAGCCGCAAG 23669
QY 1729 GGCAGCATCCAGATCCAGCCCGCGGCTTCTACTGTGATCGTGATGCAAGTGGCAAC 1788
Db 23670 GGCAGCATCCAGATCCAGCCCGCGGCTTCTACTGTGATCGTGATGCAAGTGGCAAC 23729
QY 1789 CAGTACAGCGCTTCGACGGAGCCCTGGACGGGCTTAACCTCCGGGACAGCTTGCAAG 1848
Db 23730 CAGTACAGCGCTTCGACGGAGCCCTGGACGGGCTTAACCTCCGGGACAGCTTGCAAG 23789
QY 1849 GTGGGTGTCTTCTGGACTATGACCAAGGCTTGCTCATCTTCTACATGCTGATGACATG 1908
Db 23790 GTGGGTGTCTTCTGGACTATGACCAAGGCTTGCTCATCTTCTACATGCTGATGACATG 23849
QY 1909 TCTGGCTCTPACACCTTCCCGGAGAGTTCCTCGGCAAGCTCTGCTCTTACTTCAGGCCT 1968
Db 23850 TCTGGCTCTPACACCTTCCCGGAGAGTTCCTCGGCAAGCTCTGCTCTTACTTCAGGCCT 23909
QY 1969 GGCACAGCCACCCCAATGCAAGAGCTTCAGCCGCTGGGATCAACACCGTCCGATC 2028
Db 23910 GGCACAGCCACCCCAATGCAAGAGCTTCAGCCGCTGGGATCAACACCGTCCGATC 23969

QY 2029 TAGTCCAGGAGAGGAGACACACACCTCTCGGGACCACTGCCACCTGCAAGAGCCCTGC 2088
DB 23970 TAGTCCAGGAGAGGAGACACACACCTCTCGGGACCACTGCCACCTGCAAGAGCCCTGC 24029
QY 2089 CCAGGAAGATAGAGACCTGGACTCCAGCCCACTGGGCCACTGGAGACCTCAGGCCAGT 2148
DB 24030 CCAGG-AGATAGAGACCTGGACTCCAGCCCACTGGGCCACTGGAGACCTCAGGCCAGT 24088
QY 2149 TGTATTACCTCCAGCCTCAGTCTGTGTAAATGGAGGTTGCATTCCTACTCTTAACTC 2208
DB 24089 TGTATTACCTCCAGCCTCAGTCTGTGTAAATGGAGGTTGCATTCCTACTCTTAACTC 24148
QY 2209 TCTTCCAGCATGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCTTTGATCCAGG 2268
DB 24149 TCTTCCAGCATGATGTTCTGTAGCTCTGACCTTGATAGGGATACAGCTTTGATCCAGG 24208
QY 2269 ATGTGACATGGTCTTCTCTCAGGGCAACCCCTGCCCCAACCCCTCATCCCCATCTTCTCAGG 2328
DB 24209 ATGTGACATGGTCTTCTCTCAGGGCAACCCCTGCCCCAACCCCTCATCCCCATCTTCTCAGG 24268
QY 2329 GGCAGGGACCTACCTTCCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTGAG 2388
DB 24269 GGCAGGGACCTACCTTCCAGTGTCTCCCTCCAGCCGAGCCCTGACCTCAGGAAGTGTGAG 24328
QY 2389 AGCATGGCCAGTGTGGCAGCCCGAAAGACACACAGCACCTCTTATGTCCCATGGCT 2448
DB 24329 AGCATGGCCAGTGTGGCAGCCCGAAAGACACACAGCACCTCTTATGTCCCATGGCT 24388
QY 2449 AAGACTTACCCCTGACCAAGCTAGTGTGGGCACTTACCCCTGACCCCACTCCACAGTG 2508
DB 24389 AAGACTTACCCCTGACCAAGCTAGTGTGGGCACTTACCCCTGACCCCACTCCACAGTG 24448
QY 2509 GTCCAGAGTGTACCTGTGCTCAGGTTGCTGAGGCAACCTCTCTGACACCCCTC 2568
DB 24449 GTCCAGAGTGTACCTGTGCTCAGGTTGCTGAGGCAACCTCTCTGACACCCCTC 24508
QY 2569 ACCAAGACTATATGTTCTTCTCTCCACTGATCTGCTGCTGATGATGCTGTG 2628
DB 24509 ACCAAGACTATATGTTCTTCTCTCCACTGATCTGCTGCTGATGATGCTGTG 24568
QY 2629 GCTGTGGAAGCACCCTGTGATGTCACACATTAATGATGTCACACCTTCC 2688
DB 24569 GCTGTGGAAGCACCCTGTGATGTCACACATTAATGATGTCACACCTTCC 24628
QY 2689 TGCCACAGGCGCAGGACAGGTTAGGTTATACCAAGCTGATGACAGGCCATTAGC 2748
DB 24629 TGCCACAGGCGCAGGACAGGTTAGGTTATACCAAGCTGATGACAGGCCATTAGC 24688
QY 2749 CTAAAGCAACTGCAGGACCAAGCCTCCCTGGATGATCGAGGTCCCGAGTCTTGAACA 2808
DB 24689 CTAAAGCAACTGCAGGACCAAGCCTCCCTGGATGATCGAGGTCCCGAGTCTTGAACA 24748
QY 2809 AGAGTCCAGCCCAACCTCTTACGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTC 2868
DB 24749 AGAGTCCAGCCCAACCTCTTACGCCAGGCTCTGTGACCTGTAGGTCAGAGGCTTC 24808
QY 2869 CAGAAGCAGTTGTTGTAATAGGACCAAGCACTGGAGGGCTGTGCTAGACCCCTT 2928
DB 24809 CAGAAGCAGTTGTTGTAATAGGACCAAGCACTGGAGGGCTGTGCTAGACCCCTT 24868
QY 2929 GTCCAGCTTGGCATCTATCTCAGTTAGGATCTGCTGACAGAAACCAAGACCACTGTAG 2988
DB 24869 GTCCAGCTTGGCATCTATCTCAGTTAGGATCTGCTGACAGAAACCAAGACCACTGTAG 24928
QY 2989 CTGGTTTAAATTAGCAAGGATTTACTCTGCGCCCTGTGGCTTGCAAAATTTGTTGAA 3048
DB 24929 CTGGTTTAAATTAGCAAGGATTTACTCTGCGCCCTGTGGCTTGCAAAATTTGTTGAA 24988
QY 3049 GAGCTGGAGACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATGCT 3108
DB 24989 GAGCTGGAGACAGACTCTGCTGAATTTCCAGGAATCTCCAGCGCCAGATTCATGCT 25048
QY 3109 CTGTTGTGACCAAGAGCTGCCCCCATCTGACAGGAAGCACTATGCCAGGAAGCTGCTG 3168

DB 25049 CTGTTGTGACAGGAAGCTGCCCCATCTGCAGGAAGCCACTATGCCAGAAAGCTGCTG 25108
QY 3169 ACTGAGAACTAGGCTCCCTCTGCGACCGTCCGTCCAGCCCAATAGATGTCTCGAGGCT 3228
DB 25109 ACTGAGAACTAGGCTCCCTCTGCGACCGTCCGTCCAGCCCAATAGATGTCTCGAGGCT 25168
QY 3229 GCCCTCTCCCACTTCACTCAGTTCCCAAACTAAATTTTACAAGAGATCTGTTGGG 3288
DB 25169 GCCCTCTCCCACTTCACTCAGTTCCCAAACTAAATTTTACAAGAGATCTGTTGGG 25228
QY 3289 GGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCAATTCCT 3348
DB 25229 GGAATTAAGTCAGATCCAGAACCTTGGCTGCAAGGAGTCTGGGAAATGTCAATTCCT 25288
QY 3349 AGAAGAACTAGGTTGGTGGTGGAGCAAGCCCACTCTGCGTTTTCTGCCACAGATCCAA 3408
DB 25289 AGAAGAACTAGGTTGGTGGTGGAGCAAGCCCACTCTGCGTTTTCTGCCACAGATCCAA 25348
QY 3409 TCGTGAAGAACTCGGAGAGGTTGAGTCCACATCTAGGTTGTCTGCCCTTGGCTCT 3468
DB 25349 TCGTGAAGAACTCGGAGAGGTTGAGTCCACATCTAGGTTGTCTGCCCTTGGCTCT 25408
QY 3469 ATCCCTGCGCCAGAGTGGGAACTGGAGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCC 3528
DB 25409 ATCCCTGCGCCAGAGTGGGAACTGGAGAGTGGGCTGCAAGACTGAGCCTAAATGTCTCC 25468
QY 3529 CCGGCTGTGACTTTCTTTCTAGTCTCTGGGCTAGATTCTGCACTTGGGTTCTTGACA 3588
DB 25469 CCGGCTGTGACTTTCTTTCTAGTCTCTGGGCTAGATTCTGCACTTGGGTTCTTGACA 25528
QY 3589 CACACACCTCCCAAGTAGCCGGAAGACTAAACACAGGGGTTCTTAAATGGCTG 3648
DB 25529 CACACACCTCCCAAGTAGCCGGAAGACTAAACACAGGGGTTCTTAAATGGCTG 25588
QY 3649 CCGGCTGCGCCAGGCTCTCCCTTGGGCAAAAGAAATGTGTCAGCCCTACCCCAACCTTCAA 3708
DB 25589 CCGGCTGCGCCAGGCTCTCCCTTGGGCAAAAGAAATGTGTCAGCCCTACCCCAACCTTCAA 25648
QY 3709 CTACAGAACTCGGCGCCACCCAGCAGTATTTTATTTAAATGTGTCAGTTTATGAG 3768
DB 25649 CTACAGAACTCGGCGCCACCCAGCAGTATTTTATTTAAATGTGTCAGTTTATGAG 25708
QY 3769 TTATCATCAATTTGTAATTAATTAAGTTACAGATGTCA 3807
DB 25709 TTATCATCAATTTGTAATTAATTAAGTTACAGATGTCA 25747

RESULT 7
AAK80625
ID AAK80625 standard; DNA; 5866 BP.
XX
AC AAK80625;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35437.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
FN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.

CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 5866 BP; 1464 A; 1580 C; 1489 G; 1333 T; 0 U; 0 Other;

Query Match 60.3%; Score 2306.2; DB 4; Length 5866;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2330; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY	1473	CCACCAGTGCAGCGCCCTAACCTCGACCCGGGCACAGCCACAGCGGCTGATCCT	1532
DB	1	CCCCAGTGCAGCGCCCTAACCTCGACCCGGGCACAGCCACAGCGGCTGATCCT	50
QY	1533	GTCCGACGATGACCATTTGGTTCAGGCAATTCAGGCAATTCACCCACAGCCACTCAGGACTC	1592
DB	61	GTCCGACGATGACCATTTGGTTCAGGCAATTCAGGCAATTCACCCACAGCCACTCAGGACTC	120
QY	1593	GCCAAAGCGCTTCGATGTGGAGGTGTGGTGTGGTTCGAGGCTTGAAGCTTCAGTAGTGGGT	1652
DB	121	GCCAAAGCGCTTCGATGTGGAGGTGTGGTGTGGTTCGAGGCTTGAAGCTTTCAGTAGTGGGT	180
QY	1653	CCACTACTGGAGGTGGTGTGGCGAGAGAGCCAGTGGGTGATCGGGCTCGCACAGA	1712
DB	181	CCACTACTGGAGGTGGTGTGGCGAGAGAGCCAGTGGGTGATCGGGCTCGCACAGA	240
QY	1713	AGCCGCAAGCGCAAGGGCAGCATCCAGATCCAGCCCGACCGCGGCTTCTACTGATCGT	1772
DB	241	AGCCGCAAGCGCAA-GGCAGCATCCAGATCCAGCCCGACCGCGGCTTCTACTGATCGT	299
QY	1773	GATGACGATGCAACCACTGATGAGCGCTGCAGGAGCCCTGCAGCGGCTTAAAGTCGG	1832
DB	300	GATGACGATGCAACCACTGATGAGCGCTGCAGGAGCCCTGCAGCGGCTTAAAGTCGG	359
QY	1833	GGCAAGCTTGCAAGGTGGGTGTCTCTGGACTATGACCAAGGCTTGTCTCATCTTCTA	1892
DB	360	GGCAAGCTTGCAAGGTGGGTGTCTCTGGACTATGACCAAGGCTTGTCTCATCTTCTA	419
QY	1893	CAATGCTGATGACATGTCTGGCTCTACACCTTCGCGAGAGTTCCTTGGCAAGCTCTG	1952
DB	420	CAATGCTGATGACATGTCTGGCTCTACACCTTCGCGAGAGTTCCTTGGCAAGCTCTG	479
QY	1953	CTCTTACTTCAGCCCTGGCCAGCCACCCCAATGCGAGACGTTTCAGCCCTCGGGAT	2012
DB	480	CTCTTACTTCAGCCCTGGCCAGCCACCCCAATGCGAGACGTTTCAGCCCTCGGGAT	539
QY	2013	CAACACCGTCCGCATCTAGTCCAGGAGAGAGACCAACCTCTCTGGGACCACTGCCA	2072
DB	540	CAACACCGTCCGCATCTAGTCCAGGAGAGAGACCAACCTCTCTGGGACCACTGCCA	599
QY	2073	CTTGCAAGACCGCTGCCAGGAGATAGAAAGACCTTGGATCCAGGCCCACTGGGCCACTG	2132
DB	600	CTTGCAAGACCGCTGCCAGGAGATAGAAAGACCTTGGATCCAGGCCCACTGGGCCACTG	658
QY	2133	GAGACTCAGGCGAGTTGTTTACCTTCAGCCCTCAGCTCTGTAAATGAGGTTCGATTC	2192
DB	659	GAGACTCAGGCGAGTTGTTTACCTTCAGCCCTCAGCTCTGTAAATGAGGTTCGATTC	718
QY	2193	CTTACTTCTAAACTCTCTTCAGACATCGATGTTCTGTAGCTCTGACCTTTGATAGGATA	2252
DB	719	CTTACTTCTAAACCTCTCTTCAGACATCGATGTTCTGTAGCTCTGACCTTTGATAGGATA	778

QY	2253	CAGCTTTGATCCAGGATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCTCA	2312
DB	779	CAGCTTTGATCCAGGATGTGACATGGCTTCTCTCAGGGCAACCCCTGCCCAACCTCA	838
QY	2313	TCCCATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGA	2372
DB	839	TCCCATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGA	898
QY	2373	CCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTTGGCAGGCCGGAAGACACACAGCCCTC	2432
DB	899	CCTCAGGAAGTGTCCAGAGCATGGCCAGTAGTTGGCAGGCCGGAAGACACACAGCCCTC	958
QY	2433	TTATGTCCTCCTTACAGCTTACCTCCCTGACCAAGCTAGTGTGATGGGCGATTTACCTTG	2492
DB	959	TTATGTCCTCCTTACAGCTTACCTCCCTGACCAAGCTAGTGTGATGGGCGATTTACCTTG	1018
QY	2493	ACCCAGTCCACAGTGTTCACAGGTAGTACCTGGTCTCCTAGGTTCCCTGAGAGCCAACT	2552
DB	1019	ACCCAGTCCACAGTGTTCACAGGTAGTACCTGGTCTCCTAGGTTCCCTGAGAGCCAACT	1078
QY	2553	CTCTGCCCCACCCACACCAAGAACTATATGTTCTTCTTCTCCCACTGATCTCTGGT	2612
DB	1079	CTCTGCCCCACCCACACCAAGAACTATATGTTCTTCTTCTCCCACTGATCTCTGGT	1138
QY	2613	CAGTATGATGTGTGGCTGTGGAGGACCTGGTAGTTCAGTTCACACATTATAGTCA	2672
DB	1139	CAGTATGATGTGTGGCTGTGGAGGACCTGGTAGTTCAGTTCACACATTATAGTCA	1198
QY	2673	TGTGCCACACCTTCTCTCCACAGGCGAGGACAGGTGAGGTATACCCCAAGCTGA	2732
DB	1199	TGTGCCACACCTTCTCTCCACAGGCGAGGACAGGTGAGGTATACCCCAAGCTGA	1258
QY	2733	TGCAGAGCCCAATTAGCTTAAAGCAACTGCAGGCAAGCCCTCCCTGGATGATCGAGTCC	2792
DB	1259	TGCAGAGCCCAATTAGCTTAAAGCAACTGCAGGCAAGCCCTCCCTGGATGATCGAGTCC	1318
QY	2793	CAGTAGCTCTGAAACAAGTCCAGCAACCTCTTCAGCAGGCTCTGTGACCTGCTA	2852
DB	1319	CAGTAGCTCTGAAACAAGTCCAGCAACCTCTTCAGCAGGCTCTGTGACCTGCTA	1378
QY	2853	GGGTGCAGAGGCTTCCAGAGCAGTGTGTAAATTAGGACCAAGCACTGGGAGGGCT	2912
DB	1379	GGGTGCAGAGGCTTCCAGAGCAGTGTGTAAATTAGGACCAAGCACTGGGAGGGCT	1438
QY	2913	GTGGCTAGACCCCTGTGACATTTGGCATCTATCTCAGTTAGGATCTGTGTCAGAAAA	2972
DB	1439	GTGGCTAGACCCCTGTGACATTTGGCATCTATCTCAGTTAGGATCTGTGTCAGAAAA	1498
QY	2973	GAAGAGCCACTGTAGCTGGTTTAAATTAGACAGGATTTACTACCTGGCCCTGGTGGCT	3032
DB	1499	GAAGAGCCACTGTAGCTGGTTTAAATTAGACAGGATTTACTACCTGGCCCTGGTGGCT	1558
QY	3033	TGCAAAATTTGTGGAAGAGCTGGAGAAGCAGACTCTGCTGAATTTCCAGGAACTCCACG	3092
DB	1559	TGCAAAATTTGTGGAAGAGCTGGAGAAGCAGACTCTGCTGAATTTCCAGGAACTCCACG	1618
QY	3093	GCCAGATTCATCATCTGTGTGACAGGAAAGTGTGCCCCCATCTGCAAGAGGCACTA	3152
DB	1619	GCCAGATTCATCATCTGTGTGACAGGAAAGTGTGCCCCCATCTGCAAGAGGCACTA	1678
QY	3153	TGCCAGAAAGCTGTGACTGACAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCAT	3212
DB	1679	TGCCAGAAAGCTGTGACTGACAGAACTAGGCTCCCTCTGCCACGGTCCGTGCCAGCCAT	1738
QY	3213	AGATGTCTGAGCCCTGCCCCCTCTCCCACTTCACCTCAGTTCCCAATCTTAAATTTTACA	3272
DB	1739	AGATGTCTGAGCCCTGCCCCCTCTCCCACTTCACCTCAGTTCCCAATCTTAAATTTTACA	1798
QY	3273	AGAGATTCTGTTGGGGAACTTAAAGTCAGATCCAGAACTTTGGGTGCAAGGAGTCTGG	3332
DB	1799	AGAGATTCTGTTGGGGAACTTAAAGTCAGATCCAGAACTTTGGGTGCAAGGAGTCTGG	1858

QY 1849 GTGGGTGTCCTTGGACTATGACAAAGGCTTGCTCACTTCTTCAATGCTGATGACATG 1908
Db 22326 GTGGGTGTCCTTGGACTATGACAAAGGCTTGCTCACTTCTTCAATGCTGATGACATG 22385
QY 1909 TCCTGGCTCTACACTTCCGCGAGAGTTCCCTGCGAAGCTCTGCTTCTTACTTTCAGCCCT 1968
Db 22386 TCCTGGCTCTACACTTCCGCGAGAGTTCCCTGCGAAGCTCTGCTCTTACTTCTTAGCCCT 22445
QY 1969 GGCAGAGCCACGCAATGCGAAGAACTTTCAGCGCTGCGGATCAACACCGTCGCAATC 2028
Db 22446 GGCAGAGCCACGCAATGCGAAGAACTTTCAGCGCTGCGGATCAACACCGTCGCAATC 22505
QY 2029 TAGTCCAGGAGAGGAGACCAACACTTCTGGGACCACTGCGCACTTCCAGAGCCCTGC 2088
Db 22506 TAGTTCAGGAGAGGAGAAACACAA-CTCTCTGGGAACTGCGCACTTCCAGAGCCCTGC 22564
QY 2089 CCAGGACATAGAGACCTGGACTCCAGCCACCGTGGCCACTGCGAGACCTCAGGCCAGT 2148
Db 22565 CCAGG-AGATAGAAACCTGGACTCCAGCCACCGTGGCCACTGCGAGACCTCAGGCCACT 22623
QY 2149 TGTTTACCTCCAGCCTCCAGTCTGTAAATGGAGGTTGCATTCCTCTACTTCTTAAACTC 2208
Db 22624 TGTTTACCTCCAGCCTCCAGTCTGTAAATGGAGGTTGCATTCCTCTACTTCTTAAACTC 22683
QY 2209 TCTTCAGCATGATGTTCTGTAGCTCTGACCTTGATAGGATACAGCTTTGATCCAAAG 2268
Db 22684 TCTTCAGCATGATGTTCTGTACCTCTGACCTTGATAGGAAACAGCTTTGATCCAAAG 22743
QY 2269 ATGTGACATGGCTTCTCTCAGGCAACCCCTGCCCACTCATCCCTCTCTCTCAGG 2328
Db 22744 ATGTGACATGGCTTCTCTCAGGCAACCCCTGCCCACTCATCCCTCTCTCTCAGG 22803
QY 2329 GGCAGGGAGTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGAG 2388
Db 22804 GGCAGGGAGTACCTTCCAGTGTCTCCCTCCAGCCAGCCCTGACCTCAGGAAGTGTGAG 22863
QY 2389 AGCATGGCCAGTAGTGTGGCAGCCCGAAGACACACAGCACCTCTTATGTCCCATGGCT 2448
Db 22864 AGCATGGCCAGTAGTGTGGCAGCCCGAAGACACACAGCACCTCTTATGTCCCATGGCT 22923
QY 2449 AAGACTTACCTCCAGCTAGTGTGGGCACTTACCTTGACCCCACTCCACAGT 2508
Db 22924 AAGACTTACCTCCAGCTAGTGTGGGCACTTACCTTGACCCCACTCCACAGT 22983
QY 2509 GTACAGGTAGTACCTGTGCTTCCCTCCAGCCAGCCCTGACCTCAGGAGCCCTCCAC 2568
Db 22984 GTACAGGTAGTACCTGTGCTTCCCTCCAGCCAGCCCTGACCTCAGGAGCCCTCCAC 23043
QY 2569 ACCAAGAACTATATGGTTCCTACTTCTCCACTGTACTCTGCTGATGATGCTGTG 2628
Db 23044 ACCAAGAACTATATGGTTCCTACTTCTCCACTGTACTCTGCTGATGATGCTGTG 23103
QY 2629 GCTGTGGAAGCACCTGCTGTAGTGTCCACACATATAGTGTGACCACTTCC 2688
Db 23104 GCTGTGGAAGCACCTGCTGTAGTGTCCACACATATAGTGTGACCACTTCC 23163
QY 2689 TGCCCAAGCCGAGGACAGGCTGAGGATATACCAAGCTGATGACAGGCCCTTAGC 2748
Db 23164 TGCCCAAGCCGAGGACAGGCTGAGGATATACCAAGCTGATGACCAAGCCCTTAGC 23223
QY 2749 CTAAAGAACTGCAGGACAAAGCTCCCTGGATGATGAGGTCCTCAGTAGCTCTGAACA 2808
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QY 2809 AGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTC 2868
Db 23284 AGAGTCCAGCAACCTCTTTCAGCCAGGCTCTGTGACCTGTAGGCTGAGGAGGCTTC 23343
QY 2869 CAGAAAGCTGTGTGTAAATPAGAACCAAGCACT-GGGAGGGCTGTGGCTTAGACCCCT 2927
Db 23344 CAGAAAGCTGTGTGTAAATPAGAACCAAGCACTGGGGAGGGCTGTGGCTAAACCCCT 23403
QY 2928 TGTGACACTTGGCATCTATCTCAGTTAGGATCTGTGCGAGAAACAAAGAGCCACTTGTA 2987

Db 23404 TGTGACACTTGGCACTTATCTCAGTTAGATCTTGCTGCAGAAACAAAGAGCCACTTGTA 23463
QY 2988 GCTGTTTAAATTAGCAAGGATTTTACTACCTGGCCCTTGTTGGCTTGCAAAATTTGTTGA 3047
Db 23464 GCTGTTTAAATTAGCAAGGATTTTACTACCTGGCCCTTGTTGGCTTGCAAAATTTGTTGA 23523
QY 3048 AGAGCTGAGAGAGACACTCTGCTGAATTTTCCAGGAATCCAGGCCAGATTCATCATG 3107
Db 23524 AGAGCTGAGAGAGACACTCTGCTGAATTTTCCAGGAATCCAGGCCAGATTCATCATG 23583
QY 3108 TCTGTTGTGACACAGAAAGCTGCCCCATCTGCGAGAAAGCCACTATGCCAGAAAGCTGCT 3167
Db 23584 TCTGTTGTGACACAGAAAGCTGCCCCATCTGCGAGAAAGCCACTATGCCAGAAAGCTGCT 23643
QY 3168 GACTGCGAAACTAGGCTCCCTCTGCGACCGTCCGTCGCGCAAGATAGATGCTCAGGCC 3227
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QY 3228 TGCCCTCTCCACTTCACTCAGTTCCCAATCTTAAATTTTACAGAGATTTCTGTTGG 3287
Db 23704 TGCCCTCTCCACTTCACTCAGTTCCCAATCTTAAATTTTACAGAGATTTCTGTTGG 23763
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QY 3348 TAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCACTCGGTTTTTCTGCGCACAGCATCA 3407
Db 23824 TAGAAGGAAGTTAGGTTGGTGGAGCAAGCCCACTCGGTTTTTCTGCGCACAGCATCA 23883
QY 3408 ATCGTGAAGAACTCGGAGAGGTTGGAGTCCACATCTAGGTTGCTGCGCCCTTGGCTC 3467
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QY 3468 TATCCCTGCGCAGAGTGGGAACTGGAGAGTGGCTGCAAGCTGAGCTTAAATGTCTC 3527
Db 23944 TATCCCTGCGCAGAGTGGGAACTGGAGAGTGGCTGCAAGCTGAGCTTAAATGTCTC 24003
QY 3528 CCGGCTCTGACTTTTCTTCTAGTCTGCGGGCTTAGATTTCTGCACTTGGGGTCTCTGAC 3587
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QY 3588 ACAACACACCACTCCCAAGTAGCCGGAAGAGCTTAAACACAGGGGTTCTTAAATGGCTG 3647
Db 24064 ACAACACACCACTCCCAAGTAGCCGGAAGAGCTTAAACACAGGGGTTCTTAAATGGCTG 24123
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Db 24124 CCGGCGCCACCGGGCTCCCTTGGGCAAAAGGAATTTGTACGCCCTTACCCCAACCTTCA 24183
QY 3708 ACTACAGAACTCGGCGCACCCAGAGATTTTATTTTAAATAGTGGCCATTTATGA 3767
Db 24184 ACTACAGAACTCGGCGCACCCAGAGATTTTATTTTAAATAGTGGCCATTTATGA 24243
QY 3768 GTTATGATCAATTTGATTTAAATTTAAAGTTACAGATGTCA 3807
Db 24244 GTTATGATCAATTTGATTTAAATTTAAAGTTACAGATGTCA 24283

RESULT 9

AAK80626

ID AAK80626 standard; DNA; 5858 BP.

XX AAK80626;

XX AC

XX DT

XX 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35438.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytotstatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.
XX WC200157182-A2.
PN 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR XX (HUMA-) HUMAN GENOME SCI INC.
PR FA

XX	Rosen CA, Barash SC, Ruben SM;
PI	WPI; 2001-483426/52.
XX	
DR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT	useful for preventing, diagnosing and/or treating cancers and metastasis.
XX	
PS	Disclosure; SEQ ID NO 35438; 307lpp + Sequence Listing; English.
XX	
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	proteins and polynucleotides may be used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate (I) expression. For
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patients own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting the
CC	nucleic acids into a host cell and culturing the cell to express the
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC	represent sequences used in the exemplification of the present invention
XX	
SQ	Sequence 5858 BP; 1481 A; 1575 C; 1462 G; 1340 T; 0 U; 0 Other;
Query Match 58.9%; Score 2252; DB 4; Length 5858;	
Best Local Similarity 98.6%; Pred. No. 0;	
Matches 2303; Conservative 0; Mismatches 30; Indels 3; Gaps 3;	
QY	1473 CCACCCAGTGCACGCGCCTAACCTTGACCCGGGCACAGGCCACAGCGCGTCATCCT 1532
DB	1 CCCCAAGTGCACGCGCCTAACCTTGACCCGGGCACAGGCCACAGCGCGTCATCCT 60
QY	1533 GTCCGACGACTGCACCATTGTGGCTTACGGCACTTGACCCACAGCCACTGCAGGACTC 1592
DB	61 GTCCGACGACTGCACCATTGTGGCTTACGGCACTTGACCCACAGCCACTGCAGGACTC 120
QY	1593 GCACAACGCTTCGATGTGAGGTGTCCGGTCTGCGGTTCTGAAGCCTTCAGTAGTGGCGT 1652
DB	121 GCCAAGCGCTTCGATGTGAGGTGTCCGGTCTGAAGCCTTCAGTAGTGGCGT 180
QY	1653 CCACACTGGGAGGTGTGTGGCGGAGAAGACCAGTGGGTGATGGGCTGGCACACGA 1712
DB	181 CCACACTGGGAGGTGTGTGGCGGAAAAAACCAGTGGGTGATGGGCTGGCACACAA 240
QY	1713 AGCCGCAAGCCGCAAGGGCAGCATCCAGATCCAGCCACAGCCGGGCTTCTACTGCATCGT 1772
DB	241 AGCCGCAAGCCGCAAGGGCAGCATCCAAATCCAGCCACAGCCGGGCTTCTACTGCATCGT 300
QY	1773 GATGCAAGTGGCAAACAGTACACGCGCTGCACGGAGCCCTGGACCGGCTTAACGFCGG 1832
DB	301 GATGCAAGTGGCAAACAGTACACGCGCTGCACGGAGCCCTGCACGGAGGCTTAACGFCGG 360
QY	1833 GGACAAGCTTTGACAAGGTGGGTGTCTTCCTGGACTATGACCAAGGCTTGCTCATCTTTCTA 1892
DB	361 GGACAAGCTTTGACAAGGTGGGTGTCTTCCTGGACTATGACCAAGGCTTGCTCATCTTTCTA 420
QY	1893 CAATGCTGATGACATGTCCTGGCTCTACACCTTCGGGAGAAAGTTCCCTGGCAAGCTCTG 1952
DB	421 CAATGCTGATGACATGTCCTGGCTCTACACCTTCGGGAGAAATCCCTGGCAAGCTCTG 480
QY	1953 CTCTTACTTTCAGCCCTGGCCAGACCCACGCAATGGCAAGAACTTCAGCCGCTGCGGAT 2012
DB	481 CTCTTACTTTCAGCCCTGGCCAGACCCACGCAATGGCAAGAACTTCAGCCGCTGCGGAT 540
QY	2013 CAACACCGTCCGCATCTAGTCCAGGCAGAGGAGACCAACCTCTCTGGGACCACTGCCA 2072
DB	541 CAACACCGTCCGCCTTTAGTTTCAGGCAGAGGAGAACACAA - CTCCTGGAACTCACTGCCA 599

2073	QY	CTGCGAAGAGCCCTGCCAGGAAGATAGAAGACCTGGACCTCCAGACCCACCGTGGCCACTG	2133
600	Db	CCTGCAAGAGCCCTGCCAGG-AGATAGAAAACTCGACTCCAGCCACACCGTGGCCACTG	658
2133	QY	GAGACCTCAGGCCAGTTGTTTACCCCTCCAGCCTCCAGTCTGTAAAAATTGAGGTTGCATTTC	2192
659	Db	GAGACCTCAGGCCACTTTGTTTACCCCTCCAGCCTCCAGTCTGTAAATATGAGGTTGCATTTC	718
2193	QY	CCTACTCTCTAAACTCTCTTCCAGCATCGATGTTCTGTACCTCTGACTTGTATAGGGAATA	2252
719	Db	CCTACTCTCTAAACTCTCTTCCAGCATCGATGTTCTGTACCTCTGACTTGTATAGGGAATA	778
2253	QY	CAGCTTTGATCCAAAGATGTGACATGGCTCTCCTCAGGGCAACCCCTGCCACACCTCTCA	2312
779	Db	CAGCTTTGATCCAAAGATGTGACATGGCTCTCCTCAGGGCAACCCCTGCCACACCTCTCA	838
2313	QY	TCCCCATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCAGCCAGCCCTGTA	2372
839	Db	TCCCCATCTTCTCAGGGCAGGGGACTACCTTCCAGTGTCTCCCTCAGCCAGCCCTGTA	898
2373	QY	CCTCAGGAAGTGTACAGCATGGCCAGTAGTTGGCAGCCCGAAAGACACACAGCACCTTC	2432
899	Db	CCTCAGGAAGTGTACAGCATGGCCAGTAGTTGGCAGCCCGAAAGACACACAGCACCTTC	958
2433	QY	TTATGTCCCATGGCTTAAGACTTTACCCCTGACCAAGCTAGTGTAGTGCGCCATTATCCCTTG	2492
959	Db	TTATGTCCCATGGCTTAAGACTTTACCCCTGACCAAGCTAGTGTAGTGCGCCATTATCCCTTG	1018
2493	QY	ACCCAGTGTCCACAGTGGTTCACAGGTAGTACCTGGTCTTAGGGTTGCTGAGAGCCAACT	2552
1019	Db	ACCCAGTGTCCACAGTGGTTCACAGGTAGTACCTGGTCTTAGGGTTGCTGAGAGCCAACT	1078
2553	QY	CTCCTGCCACCCCCACACCAAGAACTATATGGTTTCTTACTTCTCCCACTGATCTGTGGT	2612
1079	Db	CTCCTGCCACCCCCACACCAAGAAATATATGGTTTCTTACTTCTCCCACTGATCTGTGGT	1138
2613	QY	CAGTGTATGTCTGTGGCCCTGTGGAAGGCAACCTGGTAGTTGAGTCCACATATAGTCA	2672
1139	Db	CAGTGTATGTCTGTGGCCCTGTGGAAGGCAACCTGGTAAATTGAATCCACATATAGTCA	1198
2673	QY	TGTGCCACACCTTCTTGCCCAACAGCCGAGGACAGGGTGAGGTATACCCAAAGGTGA	2732
1199	Db	TGTGCCACACCTTCTTGCCCAACAGCCGAGGACAGGGTGAGGTATACCCAAAGGTGA	1258
2733	QY	TGCAGAGCCCATTAGCCTTAAAGCAACTGCAGACACAAGCCTCCCTGATGATCGAGTGCC	2792
1259	Db	TGCAGAGCCCATTAGCCTTAAAGCAACTGCAGACACAAGCCTCCCTGATGATCGAGTGCC	1318
2793	QY	CCAGTGTACTGTGAACAGAGTCCAGCCAAACCTCTTCAGCCAGGCTCTGTGACCTGTA	2852
1319	Db	CCAGTGTACTGTGAACAGAGTCCAGCCAAACCTCTTCAGCCAGGCTCTGTGACCTGTA	1378
2853	QY	GGGTGCAGGAGGCTTCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACT-GGAGGGGC	2911
1379	Db	GGGTGCAGGAGGCTTCAGAAAGCAGTTGTTGTAATTAGGACCCCAAGCACTGGGGAGGGC	1438
2912	QY	TGTTGGCTAGACCCCTTGTGACACTTGGCATCTATCTCAGTTAGGATTCCTGCTGCAGAAA	2971
1439	Db	TGTTGGCTAAACCCCTTGTGACACTTGGCATCTATCTCAGTTAGGATTCCTGCTGCAGAAA	1498
2972	QY	ACAAGAGCCACTTGTAGCTGGTTTAATTAGACAAGGATTTACTACCTGGCCCTGGTGGC	3031
1499	Db	ACAAGAGCCACTTGTAGCTGGTTTAATTAGACAAGGATTTACTACCTGGCCCTGGTGGC	1558
3032	QY	TTGCAAAATTTGTGAAGAGCTGGAAAGCAGACTCTGCTGAATTTCCAGGAATCTCCAG	3091
1559	Db	TTGCAAAATTTGTGAAGAGCTGGAAAGCAGACTCTGCTGAATTTCCAGGAATCTCCAG	1618
3092	QY	CGCCAGATTCATATGTTCTGTTGTGACAGGAAGCTGCCCCATCTGACAGGAAGCACT	3151
1619	Db	CGCCAGATTCATATGTTCTGTTGTGACAGGAAGCTGCCCCATCTGACAGGAAGCACT	1678

QY 3152 ATGCAGAAAGCTGCTGACTGCAGAACTAG3CTCCCTCTGCGACGGTCCGTCGACGCCAA 3211
Db |||||||
QY 1679 ATGCCAGAAAGCTGCTGACTGCAGAACTAG3CTCCCTCTGCGACGGTCCGTCGACGCCAA 1738
Db |||||||
QY 3212 TAGATGTCCTGAGGCTGCGCCCTCTCCCACTTCACTCAGTTCCCAATCTAAATTTTAC 3271
Db |||||||
QY 1739 TAGATGTCCTGAGGCTGCGCCCTCTCCCACTTCACTCAGTTCCCAATCTAAATTTTAC 1798
Db |||||||
QY 3272 AAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAACTTGGCTGCGAAGGAGTCTG 3331
Db |||||||
QY 1799 AAGAGATCTGTTGGGGAACTTAAGTCAGATCCAGAACTTGGCTGCGAAGGAGTCTG 1858
Db |||||||
QY 3332 GGAATGTCATTTCCCTAGAGGAAGTGTAGGTGGGTGGAGCAGCCCACTCGCTTTT 3391
Db |||||||
QY 1859 GGAATGTCATTTCCCTAGAGGAAGTGTAGGTGGGTGGAGCAGCCCACTCGCTTTT 1918
Db |||||||
QY 3392 TCTGCCACAGATCCCAATCGTAGAAGTCTGGGAGAGGGTGGAGTCCACATCTAGGGTTG 3451
Db |||||||
QY 1919 TCTGCCACAGATCCCAATCGTAGAAGTCTGGGAGAGGGTGGAGTCCACATCTAGGGTTG 1978
Db |||||||
QY 3452 TCTGCCACAGATCCCAATCGTAGAAGTCTGGGAGAGGGTGGAGTCCACATCTAGGGTTG 3511
Db |||||||
QY 1979 TCTGCCACAGATCCCAATCGTAGAAGTCTGGGAGAGGGTGGAGTCCACATCTAGGGTTG 2038
Db |||||||
QY 3512 TGAGCCTAAATGTCCTCCCGGCTTGAATTTCTTCTAGTCTCTGGGCTTAGATTTCTGC 3571
Db |||||||
QY 2039 TGAGCCTAAATGTCCTCCCGGCTTGAATTTCTTCTAGTCTCTGGGCTTAGATTTCTGC 2098
Db |||||||
QY 3572 ACTTGGGCTCTTGACACAAACACACATCCCAAGTACCGGAGAGCTAAACACAGGGG 3631
Db |||||||
QY 2099 ACTTGGGCTCTTGACACAAACACACATCCCAAGTACCGGAGAGCTAAACACAGGGG 2158
Db |||||||
QY 3632 GTTCTTAAATGTCCTCCCGGCTTGAATTTCTTCTAGTCTCTGGGCTTAGATTTCTGC 3691
Db |||||||
QY 2159 GTTCTTAAATGTCCTCCCGGCTTGAATTTCTTCTAGTCTCTGGGCTTAGATTTCTGC 2218
Db |||||||
QY 3692 CTACCCCAACCTTCAACTACCAATCTGGGCAACCCAGCAGTATTTTATTTAAAT 3751
Db |||||||
QY 2219 CTACCCCAACCTTCAACTACCAATCTGGGCAACCCAGCAGTATTTTATTTAAAT 2278
Db |||||||
QY 3752 GTTGCCCAATTTATGAGTATGATCAATTTGTATTTAAATTAAGTTACAGATGCA 3807
Db |||||||
QY 2279 GTTGCCCAATTTATGAGTATGATCAATTTGTATTTAAATTAAGTTACAGATGCA 2334
Db |||||||

RESULT 10

ADC37266

ID ADC37266 standard; DNA; 2246 BP.

AC ADC37266;

XX

XX 18-DEC-2003 (first entry)

DT Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 99.

DE

XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;

XX cancer; infectious disease; bone disease; AIDS;

XX neurodegenerative disease; ischaemic disorder; Antiinflammatory;

XX immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;

XX Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.

XX Homo sapiens.

XX

XX WC2003048202-A2.

XX 12-JUN-2003.

XX

XX 03-DEC-2002; 2002WO-JP012644.

XX

XX 03-DEC-2001; 2001JP-00368692.

XX

XX 05-DEC-2001; 2001US-0335829P.

XX

XX 03-OCT-2002; 2002JP-00291302.

XX

XX 04-OCT-2002; 2002US-0415769P.

XX (ASAH) ASahi KASEI KK.

XX Matsuda A, Muramatsu S;

XX WPI; 2003-505282/47.

XX P-PSDB; ADC37267.

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XX The present invention relates to novel proteins and their coding
sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
kappaB). The proteins and their coding sequences are useful for treating
a disease associated with NF-kappaB activation, such as inflammation,
autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
neurodegenerative diseases, or ischaemic disorders.

Claim 4; SEQ ID NO 99; 938pp; English.

Sequence 2246 BP; 418 A; 805 C; 623 G; 400 T; 0 U; 0 Other;

Query Match 45.6%; Score 1745.2; DB 9; Length 2246;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AGGTCGCTGGACCGAAGCGGTGGTGTCTAAGCTCGCGGGGTAAGGGTTCGCGTGGG 60
Db |||||||
QY 7 AGGTCGCTGGACCGAAGCGGTGGTGTCTAAGCTCGCGGGGTAAGGGTTCGCGTGGG 66
Db |||||||
QY 61 CGAGGTTTGGGCGCGGGATCCCGCAGCTGAGGGGCGGCGCCCTCTCTCTGCGC 120
Db |||||||
QY 67 CGAGGTTTGGGCGCGGGATCCCGCAGCTGAGGGGCGGCGCCCTCTCTCTGCGC 126
Db |||||||
QY 121 GGTACAGCAATGTAGCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 180
Db |||||||
QY 127 GGTACAGCAATGTAGCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 186
Db |||||||
QY 181 GCTTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 240
Db |||||||
QY 187 GCTTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 246
Db |||||||
QY 241 CGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 300
Db |||||||
QY 247 CGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 306
Db |||||||
QY 301 CTTCCCGCTCAGGATCTCCGCTCCGCTCAGCGCTCAGCGCTCCTCCAGCGCCCATCGCC 360
Db |||||||
QY 307 CTTCCCGCTCAGGATCTCCGCTCCGCTCAGCGCTCAGCGCTCCTCCAGCGCCCATCGCC 366
Db |||||||
QY 361 TTGAGTGGCCATCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 420
Db |||||||
QY 367 TTGAGTGGCCATCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 426
Db |||||||
QY 421 GCGCACCTCTCTCGGTTACCTCTCTCGGACACCTCTCTCGGACACCTCTCTCGGAC 480
Db |||||||
QY 427 GCGCACCTCTCTCGGTTACCTCTCTCGGACACCTCTCTCGGACACCTCTCTCGGAC 486
Db |||||||
QY 481 TCCTACCTCTCTCGGTTACCTCTCTCGGACACCTCTCTCGGACACCTCTCTCGGAC 540
Db |||||||
QY 487 TCCTACCTCTCTCGGTTACCTCTCTCGGACACCTCTCTCGGACACCTCTCTCGGAC 546
Db |||||||
QY 541 GCGCGGCTCTCTCAGCGCCCTCTCGGCTCTCGGCTCTCGGCTCTCTCGGCTCTCTG 600
Db |||||||
QY 547 GCGCGGCTCTCTCAGCGCCCTCTCGGCTCTCGGCTCTCGGCTCTCTCGGCTCTCTG 606
Db |||||||
QY 601 GCGCGGCTCTCTCAGCGCCCTCTCGGCTCTCGGCTCTCGGCTCTCTCGGCTCTCTG 660
Db |||||||
QY 607 GCGCGGCTCTCTCAGCGCCCTCTCGGCTCTCGGCTCTCGGCTCTCTCGGCTCTCTG 666
Db |||||||
QY 661 GCGCGGCTCTCTCAGCGCCCTCTCGGCTCTCGGCTCTCGGCTCTCTCGGCTCTCTG 720
Db |||||||

Db 667 GACCGGTGAGCTGGGTGCGAGCATCTACTTCTGCGCGCTGATACGGAGCACTGG 726
QY 721 GTGCGGAGGAGCGCAGCGGCCCGCGACTGCCCGAGTCCCGGCGACGTTCCCGGAG 780
Db 727 GTGCGGAGGAGCGCAGGGGCCCGCGACTGCCCGAGTCCCGGCGACGTTCCCGGAG 786
QY 781 CCGGCGTGGCGCCAGCCCTCAAGCTGGCAACATCTGTGGAGGGCTACAGCTCTCTCCG 840
Db 787 CCGGCGTGGCGCCAGCCCTCAAGCTGGCAACATCTGTGGAGGGCTACAGCTCTCTCCG 846
QY 841 CTGAGCGCATCTCAAGCGCGCGCGCGCGGCGGACCTTGCAGCGCGACGACCAAGTTC 900
Db 847 CTGAGCGCATCTCAAGCGCGCGCGCGCGGCGGACCTTGCAGCGCGACGACCAAGTTC 906
QY 901 AAGCTCTTCTGCTCTACGAGCCGCGCGCTTCTGCTTCTTCTGCGACGAGCTGCACTG 960
Db 907 AAGCTCTTCTGCTCTACGAGCCGCGCGCTTCTGCTTCTTCTGCGACGAGCTGCACTG 966
QY 961 CAGGAGCAGCATAGTTCACCGCATCTGAGCGGCTTTCGAGAGCTGCGAGGGAGCTG 1020
Db 967 CAGGAGCAGCATAGTTCACCGCATCTGAGCGGCTTTCGAGAGCTGCGAGGGAGCTG 1026
QY 1021 AAGGACCAACTTCAGGCCCTTCAAGACAGCGGCGGAACACACGAAGCGCTGCACTG 1080
Db 1027 AAGGACCAACTTCAGGCCCTTCAAGACAGCGGCGGAACACACGAAGCGCTGCACTG 1086
QY 1081 CTCAGCGCAACTGTGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATCGCG 1140
Db 1087 CTCAGCGCAACTGTGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATCGCG 1146
QY 1141 GAGGCTTTCAGCGGCTGACCGGCTGCTGCTGTAACGCCAGAGGCCATGCTAGAGGAG 1200
Db 1147 GAGGCTTTCAGCGGCTGACCGGCTGCTGCTGTAACGCCAGAGGCCATGCTAGAGGAG 1206
QY 1201 CTGAGGGGACACGCGCGCGCTGACCGCATCTGAGCAAGTTCAGCGCTACAGC 1260
Db 1207 CTGAGGGGGAACGCGCGCGCTGACCGCATCTGAGCAAGTTCAGCGCTACAGC 1266
QY 1261 CAGGAGTTCGCAAGTTCAGAGGGAGCGCGAGTCTTCCAGGAGCGGCTGCTGAAACC 1320
Db 1267 CAGGAGTTCGCAAGTTCAGAGGGAGCGCGAGTCTTCCAGGAGCGGCTGCTGAAACC 1326
QY 1321 GACCGGCACACCTTCTGCTGGGTGGCTCACTGTCGCGGCTCAAGGGAAATC 1380
Db 1327 GACCGGCACACCTTCTGCTGGGTGGCTCACTGTCGCGGCTCAAGGGAAATC 1386
QY 1381 CATGAGACCAACTCACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCGCCCTGCA 1440
Db 1387 CATGAGACCAACTCACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCGCCCTGCA 1446
QY 1441 TACACATCTGGAAGTTCCTGTTCCAGGACATCCAGCCAGTGCAGCGCCCTTACCCCTG 1500
Db 1447 TACACATCTGGAAGTTCCTGTTCCAGGACATCCAGCCAGTGCAGCGCCCTTACCCCTG 1506
QY 1501 GACCGGGCAGACGCCACAGCGCCTGATCTGTCGAGAGCTGCACCAATGTCGCTTAC 1560
Db 1507 GACCGGGCAGACGCCACAGCGCCTGATCTGTCGAGAGCTGCACCAATGTCGCTTAC 1566
QY 1561 GGCACATCTGACCCACAGCCACTGCAAGGACTGCCAAAGCGCTTCGATGTGAGGTGTGCG 1620
Db 1567 GGCACATCTGACCCACAGCCACTGCAAGGACTGCCAAAGCGCTTCGATGTGAGGTGTGCG 1626
QY 1621 GTGCTGGGTCTGAAGCCTTCACTAGTGGGTCTCACTCTGGGAGTGTGTGGCGGAG 1680
Db 1627 GTGCTGGGTCTGAAGCCTTCACTAGTGGGTCTCACTCTGGGAGTGTGTGGCGGAG 1686
QY 1681 AAGACCCAGTGGTGTATCGGCTGGCACAGAGCGCGAAGCGGAGGCGAGCATCCAG 1740
Db 1687 AAGACCCAGTGGTGTATCGGCTGGCACAGAGCGCGAAGCGGAGGCGAGCATCCAG 1746
QY 1741 ATCCAGCCAGCGCGCGC 1758

Db 1747 ATCCAGAACCTTGGCTGC 1764
RESULT 11
ADC37454
ID ADC37454 standard; DNA; 2207 BP.
XX
AC ADC37454;
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 287.
XX
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease; cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Antinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003048202-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002WO-JP012644.
XX
PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-04115769P.
XX
PA (ASAH) ASahi KASEI KK.
XX
PI Matsuda A, Muramatsu S;
XX
WPI: 2003-505282/47.
P-PSDB; ADC37455.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB), useful for treating inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases or ischemic disorders.
XX
PS Claim 4; SEQ ID NO 287; 938pp; English.
XX
CC The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-kappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.
SQ Sequence 2207 BP; 414 A; 784 C; 618 G; 391 T; 0 U; 0 Other;
Query Match 43.3%; Score 1657.2; DB 9; Length 2207;
Best Local Similarity 97.3%; Pred. No. 5e-307;
Matches 1711; Conservative 0; Mismatches 8; Indels 39; Gaps 1;
QY 1 AGGCTGCGCTGGACCAAGCGGTGCTGTAAGCTCGCGGGGTAAAGGGTGGCGTGGG 60
Db 7 AGGCTGCGCTGGACCAAGCGGTGCTGTAAGCTCGCGGGGTAAAGGGTGGCGTGGG 66
QY 61 CAGAGGTTTGGGCGCGGATCCGGAGCTGAGCGGCGCGCACCCCTCTCTCTCTGCC 120
Db 67 CAGAGGTTTGGGCGCGGATCCGGAGCTGAGCGGCGCGCACCCCTCTCTCTGCC 126
QY 121 GGTCTACAGCATGTACGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 180
Db 127 GGTCTACAGCATGTACGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT 186
QY 181 GGTCTCTGCGCTTCCCGCGCACCGCCCGGATTCGACCCCGCTTAAAGGGTCCAC 240

Db 187 GCTTCTCGCCCTCCCGCAGCCGCCACCCCGGATTTTCGACCCCTTAAGGCTCCAC 246
Qy 241 CCGCTCCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 300
Db 247 CCGCTCCGGGATCCCTTCTCCAGCTCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 306
Qy 301 CTTCCCGCTCAGGATCTCCGTCCTCAGCCGCTCAGAGCTCTCTCCAGCGCCCATCGCC 360
Db 307 CTTCCCGCTCAGGATCTCCGTCCTCAGCCGCTCAGAGCTCTCTCCAGCGCCCATCGCC 366
Qy 361 TTGAGCTGCCACTACCTCTAGACTGCCCTCCCGGCTGGCTGCCAGGAGTCTAGCC 420
Db 367 TTGAGCTGCCACTACCTCTAGACTGCCCTCCCGGCTGGCTGCCAGGAGTCTAGCC 426
Qy 421 GCGACCCCTTCTCGGCTTACCTCTCTCGGACAGCACCCCTCTCCCTTCTCGGTAGC 480
Db 427 GCGAC-----CCCTTCTCGGTAGC 447
Qy 481 TCCTACCCCTCGCTGTCGGGCTCTGTCGCCGCCAGCCCTCGGTGCTGCTCCGACAA 540
Db 448 TCCTACCCCTCGCTGTCGGGCTCTGTCGCCGCCAGCCCTCGGTGCTGCTCCGACAA 507
Qy 541 GCGCGGCTCTCTCAGCCGCCCTCTGCTGCGGCTGGGCTGGGCTGGGCTGGGCTGGG 600
Db 508 GCGCGGCTCTCTCAGCCGCCCTCTGCTGCGGCTGGGCTGGGCTGGGCTGGGCTGGG 567
Qy 601 GCCATGCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 568 GCCATGCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
Qy 661 GACCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 628 GACCGCTGAGCTGAGCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
Qy 721 GTGCGCAGAGGCGCAGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 688 GTGCGCAGAGGCGCAGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
Qy 781 CCGCGCTGGGCGCAGCTCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 840
Db 748 CCGCGCTGGGCGCAGCTCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 807
Qy 841 CTGAGCCACTCTCAACGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 808 CTGAGCCACTCTCAACGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
Qy 901 AAGCTTCTGCTCAGGACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 868 AAGCTTCTGCTCAGGACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
Qy 961 CAGGACGAGCATCAGGCTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1020
Db 928 CAGGACGAGCATCAGGCTCAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 987
Qy 1021 AAGGACCACTTCAAGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 988 AAGGACCACTTCAAGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1047
Qy 1081 CTGAGGACCACTGAGGCGGAGCAAGCTTTCACCAAGAGCTGCGGACCACTATCGGC 1140
Db 1048 CTGAGGACCACTGAGGCGGAGCAAGCTTTCACCAAGAGCTGCGGACCACTATCGGC 1107
Qy 1141 GAGGCTTTCAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1200
Db 1108 GAGGCTTTCAGGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1167
Qy 1201 CTGAGGCGGACAGGCGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1260
Db 1168 CTGAGGCGGACAGGCGCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1227
Qy 1261 CAGGAGCTGCGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
Db 1228 CAGGAGCTGCGAGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1287

Qy 1321 GACCGCACACCTTCTCGGCTGGGTGGCTCTACTGTCCAGCGGCTCAAGGGAATC 1380
Db 1288 GACCGCACACCTTCTCGGCTGGGTGGCTCTACTGTCCAGCGGCTCAAGGGAATC 1347
Qy 1381 CATGAGACCAACCTCACATATGAAGACTTCCCGACCTTCCAAAGTACACAGGCCCTCGAG 1440
Db 1348 CATGAGACCAACCTCACATATGAAGACTTCCCGACCTTCCAAAGTACACAGGCCCTCGAG 1407
Qy 1441 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACAGTGCAGCGGCCCTAACCTG 1500
Db 1408 TACACATCTGGAAGTCCCTGTTCCAGGACATCCACAGTGCAGCGGCCCTAACCTG 1467
Qy 1501 GACCGGCGACAGCCACAGCGCTGATCTCTGCGACGACTGCACCATTTGTCCTTAC 1560
Db 1468 GACCGGCGACAGCCACAGCGCTGATCTCTGCGACGACTGCACCATTTGTCCTTAC 1527
Qy 1561 GGCAACTTGCACCCACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGCG 1620
Db 1528 GGCAACTTGCACCCACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGCG 1587
Qy 1621 GTGCTGGGTTCTGAAGCTTTCAGTGTGGGCTCCTACTGTGGAGGTGTGTGGCGGAG 1680
Db 1588 GTGCTGGGTTCTGAAGCTTTCAGTGTGGGCTCCTACTGTGGAGGTGTGTGGCGGAG 1647
Qy 1681 AAGACCCAGTGGGTGATCGGCTGGCACACGACCGCAAGCGCGCAAGGCGCAGCATCCAG 1740
Db 1648 AAGACCCAGTGGGTGATCGGCTGGCACACGACCGCAAGCGCGCAAGGCGCAGCATCCAG 1707
Qy 1741 ATCCAGCCAGCGCGGC 1758
Db 1708 ATCCAGACCTTGGCTGC 1725

RESULT 12
ID ADC37264 standard; DNA; 2207 BP.
XX ADC37264;
AC ADC37264;
XX
DT 18-DEC-2003 (first entry)
XX
DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 97.
XX
KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Anti-inflammatory;
KW immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; ds.
XX
OS Homo sapiens.
XX
PN WO2003048202-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002WO-JP012644.
XX
PR 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
PA (ASAH) ASahi Kasei KK.
XX
PI Matsuda A, Muramatsu S;
DR WPI; 2003-505282/47.
DR P-PSDB; ADC37265.
XX
PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or

PT	ischemic disorders.	
XX	Claim 4; SEQ ID NO 97; 938pp; English.	
XX	The present invention relates to novel proteins and their coding sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-kappaB). The proteins and their coding sequences are useful for treating a disease associated with NF-kappaB activation, such as inflammation, autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS, neurodegenerative diseases, or ischaemic disorders.	
XX	Sequence 2207 BP; 414 A; 784 C; 618 G; 391 T; 0 U; 0 Other;	
XX	Query Match 43.3%; Score 1657.2; DB 9; Length 2207;	
XX	Best Local Similarity 97.3%; Pred. No. 5e-307; Mismatches 1711; Conservative 0; Indels 39; Gaps 1;	
QY	1 AGGCTGCGCTGACCGAAGCGGTGGTGTCTAAGCTCGCGGGGTAAAGGGTCCGCTGGG 60	841 CTGACGCGATCTCTCAACGCGCGCGCGCGCGACCTCTCCAGCGCGCACACGAGGTC 900
DB	7 AGGCTGCGCTGACCGAAGCGGTGGTGTCTAAGCTCGCGGGGTAAAGGGTCCGCTGGG 66	808 CTGACGCGATCTCTCAACGCGCGCGCGCGCGACCTCTCCAGCGCGCACACGAGGTC 867
QY	61 CAGGGTTTGGGCGCGGATCCGGAGCTGAGCGGGCCGGCACCCCTCTCTTCTCTGTC 120	901 AAGCTCTTCTGCTCTCAGCGACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
DB	67 CAGGGTTTGGGCGCGGATCCGGAGCTGAGCGGGCCGGCACCCCTCTCTTCTCTGTC 126	868 AAGCTCTTCTGCTCTCAGCGACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 927
QY	121 GGTACAGCAATGTACGGCTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180	961 CACGAGCAGCATCAGGTACCGGCTACGACGCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 1020
DB	127 GGTACAGCAATGTACGGCTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 186	928 CACGAGCAGCATCAGGTACCGGCTACGACGCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 987
QY	181 GCTTCTCGCCCTCCCGCACCGCCCGCCCGACCGCGGGATTTGACCCCGCTTAAAGGGTCCAC 240	1021 AAGGACCAACTTTCAGCGCTTCAACACAGCAGCGCGGAAACACACGAGCGCTGCAGCTG 1080
DB	187 GCTTCTCGCCCTCCCGCACCGCCCGCCCGACCGCGGGATTTGACCCCGCTTAAAGGGTCCAC 246	988 AAGGACCAACTTTCAGCGCTTCAACACAGCAGCGCGGAAACACACGAGCGCTGCAGCTG 1047
QY	241 CCGCTTCGGGATTCGCTTCTCCAGCTCTATTCCTTAGAGTGTGCTCCCGCCCTTAGAA 300	1081 CTCAAGCGCAACTCTGGCGGAGACCAAGTCTTCCACCAAGAGCTTGGGACCACTATCGGC 1140
DB	247 CCGCTTCGGGATTCGCTTCTCCAGCTCTATTCCTTAGAGTGTGCTCCCGCCCTTAGAA 306	1048 CTCAAGCGCAACTCTGGCGGAGACCAAGTCTTCCACCAAGAGCTTGGGACCACTATCGGC 1107
QY	301 CTTCCCGCTCAGGATTCGCTCCCTCAGCGCTCTCAGCGCTCTCCAGCGCGCATCGCC 360	1141 GAGGCTTTCGAGCGGCTGCACCGGCTGCTGGTGAACGCCAGAAAGCCATGCTAGAGGAG 1200
DB	307 CTTCCCGCTCAGGATTCGCTCCCTCAGCGCTCTCAGCGCTCTCCAGCGCGCATCGCC 366	1108 GAGGCTTTCGAGCGGCTGCACCGGCTGCTGGTGAACGCCAGAAAGCCATGCTAGAGGAG 1167
QY	361 TTGAGTGCCTACTAGCTAGCTGCTTCCGCTCCCGGGCTGGCTCCCGAGGCTCTCAGCC 420	1201 CTGGAGGCGGACACCGCGCGCAGCTGACCGACATCGACGAAAGTCCAGCGCTACAGC 1260
DB	367 TTGAGTGCCTACTAGCTAGCTGCTTCCGCTCCCGGGCTGGCTCCCGAGGCTCTCAGCC 426	1168 CTGGAGGCGGACACCGCGCGCAGCTGACCGACATCGACGAAAGTCCAGCGCTACAGC 1227
QY	421 GCGACCCCTTCTCGGTTACCTCTTCGGGACAGACCCCTCTTCGGGTAGC 480	1261 CAGCAGCTGCGCAAGGTCAGGAGGAGCCAGATCTCTTCAGGAGCGGTGGCTGAAACC 1320
DB	427 GCGCAC-----CCCTTCTCCGTTAGC 447	1228 CAGCAGCTGCGCAAGGTCAGGAGGAGCCAGATCTCTTCAGGAGCGGTGGCTGAAACC 1287
QY	481 TCCTACCCCTGCTGTGGGGGCTCTGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACA 540	1321 GACCGGACACCTTCTCTGGCTGGGTGGCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1380
DB	448 TCCTACCCCTGCTGTGGGGGCTCTGTCCCGCGCCAGCCCTCGGTGCTGCTCCGACA 507	1288 GACCGGACACCTTCTCTGGCTGGGTGGCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1347
QY	541 GCGCGCGCTCTCTCAGCGCGCCCTGCTCCCTTCGGGCGCCCTCTCTCTCTCTCTCTCT 600	1381 CATGAGACCAACTCACAATATGAAGACTTCCCGACTTCCCAAGTACACAGGCCCTTCGAC 1440
DB	508 GCGCGCGCTCTCTCAGCGCGCCCTGCTCCCTTCGGGCGCCCTCTCTCTCTCTCTCTCT 567	1348 CATGAGACCAACTCACAATATGAAGACTTCCCGACTTCCCAAGTACACAGGCCCTTCGAC 1407
QY	601 GCATGGGTGAGCTCTAAGACAGCTGCTGTGCTTCCATCTGCTGAGCATCTACACAG 560	1441 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCCGCCCTTAACCCCTG 1500
DB	568 GCATGGGTGAGCTCTAAGACAGCTGCTGTGCTTCCATCTGCTGAGCATCTACACAG 627	1408 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCCGCCCTTAACCCCTG 1467
QY	661 GACCGGTGAGCTGCGGTGCGAGCACTACTTCTGCGCGGCTGCTCATCAGGAGCACTGG 720	1501 GACCGGCGACAGCCCGACAGCGCTGATCTCTGTCGAGCACTGACACCATTTGSGCTTAC 1560
DB	628 GACCGGTGAGCTGCGGTGCGAGCACTACTTCTGCGCGGCTGCTCATCAGGAGCACTGG 687	1468 GACCGGCGACAGCCCGACAGCGCTGATCTCTGTCGAGCACTGACACCATTTGSGCTTAC 1527
QY	721 GTGCGCAGGAGCGCAGGGCGCCCGAGCTGCTCCCGAGTCCGGCGCACGTTTCGCCGAG 780	1561 GGCAACTTGCACCCACAGCCACTGCGAGACTCGCCAAAGCGCTTCGATGTGAGGTTGCG 1620
DB	688 GTGCGCAGGAGCGCAGGGCGCCCGAGCTGCTCCCGAGTCCGGCGCACGTTTCGCCGAG 747	1528 GGCAACTTGCACCCACAGCCACTGCGAGACTGCGCCAAAGCGCTTCGATGTGAGGTTGCG 1587
QY	781 CCGCGCTGCGCCAGCTCTAAGCTGGCGCAACATCGTGGAGGGCTACAGCTCTCTTCCCG 840	1621 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1680
DB	748 CCGCGCTGCGCCAGCTCTAAGCTGGCGCAACATCGTGGAGGGCTACAGCTCTCTTCCCG 807	1588 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1647

QY	841 CTGACGCGATCTCTCAACGCGCGCGCGCGACCTCTCCAGCGCGCACACGAGGTC 900	1561 GGCAACTTGCACCCACAGCCACTGCGAGACTCGCCAAAGCGCTTCGATGTGAGGTTGCG 1620
DB	808 CTGACGCGATCTCTCAACGCGCGCGCGCGACCTCTCCAGCGCGCACACGAGGTC 867	1528 GGCAACTTGCACCCACAGCCACTGCGAGACTGCGCCAAAGCGCTTCGATGTGAGGTTGCG 1587
QY	901 AAGCTCTTCTGCTCTCAGCGACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960	1621 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1680
DB	868 AAGCTCTTCTGCTCTCAGCGACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 927	1588 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1647
QY	961 CACGAGCAGCATCAGGTACCGGCTACGACGCGCTTCTCTCTCTCTCTCTCTCTCTCT 1020	1681 AAGACCCAGTGGGTGATCGGGCTGGCAGCACAGCGCGCAAGCGCGCAAGGCGCATCCAG 1740
DB	928 CACGAGCAGCATCAGGTACCGGCTACGACGCGCTTCTCTCTCTCTCTCTCTCTCTCT 987	1648 AAGACCCAGTGGGTGATCGGGCTGGCAGCACAGCGCGCAAGCGCGCATCCAG 1707
QY	1021 AAGGACCAACTTTCAGCGCTTCAACACAGCAGCGCGGAAACACACGAGCGCTGCAGCTG 1080	1741 ATCCAGCCCGACCGCGGC 1758
DB	988 AAGGACCAACTTTCAGCGCTTCAACACAGCAGCGCGGAAACACACGAGCGCTGCAGCTG 1047	1708 ATCCAGACCTTGGCTGC 1725
QY	1081 CTCAAGCGCAACTCTGGCGGAGACCAAGTCTTCCACCAAGAGCTTGGGACCACTATCGGC 1140	
DB	1048 CTCAAGCGCAACTCTGGCGGAGACCAAGTCTTCCACCAAGAGCTTGGGACCACTATCGGC 1107	
QY	1141 GAGGCTTTCGAGCGGCTGCACCGGCTGCTGGTGAACGCCAGAAAGCCATGCTAGAGGAG 1200	
DB	1108 GAGGCTTTCGAGCGGCTGCACCGGCTGCTGGTGAACGCCAGAAAGCCATGCTAGAGGAG 1167	
QY	1201 CTGGAGGCGGACACCGCGCGCAGCTGACCGACATCGACGAAAGTCCAGCGCTACAGC 1260	
DB	1168 CTGGAGGCGGACACCGCGCGCAGCTGACCGACATCGACGAAAGTCCAGCGCTACAGC 1227	
QY	1261 CAGCAGCTGCGCAAGGTCAGGAGGAGCCAGATCTCTTCAGGAGCGGTGGCTGAAACC 1320	
DB	1228 CAGCAGCTGCGCAAGGTCAGGAGGAGCCAGATCTCTTCAGGAGCGGTGGCTGAAACC 1287	
QY	1321 GACCGGACACCTTCTCTGGCTGGGTGGCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1380	
DB	1288 GACCGGACACCTTCTCTGGCTGGGTGGCTCACTGTCCGAGCGGCTCAAGGAAAAATC 1347	
QY	1381 CATGAGACCAACTCACAATATGAAGACTTCCCGACTTCCCAAGTACACAGGCCCTTCGAC 1440	
DB	1348 CATGAGACCAACTCACAATATGAAGACTTCCCGACTTCCCAAGTACACAGGCCCTTCGAC 1407	
QY	1441 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCCGCCCTTAACCCCTG 1500	
DB	1408 TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTCCAGCCGCCCTTAACCCCTG 1467	
QY	1501 GACCGGCGACAGCCCGACAGCGCTGATCTCTGTCGAGCACTGACACCATTTGSGCTTAC 1560	
DB	1468 GACCGGCGACAGCCCGACAGCGCTGATCTCTGTCGAGCACTGACACCATTTGSGCTTAC 1527	
QY	1561 GGCAACTTGCACCCACAGCCACTGCGAGACTCGCCAAAGCGCTTCGATGTGAGGTTGCG 1620	
DB	1528 GGCAACTTGCACCCACAGCCACTGCGAGACTGCGCCAAAGCGCTTCGATGTGAGGTTGCG 1587	
QY	1621 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1680	
DB	1588 GTGCTGGGTTCTGAAGCTTCAAGTGTGGCTGCTCACTACTGGAGGTGTTGTTGGCGGAG 1647	
QY	1681 AAGACCCAGTGGGTGATCGGGCTGGCAGCACAGCGCGCAAGCGCGCAAGGCGCATCCAG 1740	
DB	1648 AAGACCCAGTGGGTGATCGGGCTGGCAGCACAGCGCGCAAGGCGCATCCAG 1707	
QY	1741 ATCCAGCCCGACCGCGGC 1758	
DB	1708 ATCCAGACCTTGGCTGC 1725	
XX	RESULT 13	
XX	ABK12809	
XX	ID ABK12809 standard; DNA; 45845 BP.	
XX	AC ABK12809;	
XX	DT 18-JUN-2002 (first entry)	
XX		

DE Human tumour suppressor CAR-1, BAC clone RP11-150F21 5' sequence.

XX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteriophage chromosome; chromosome ip31-lp36.

XX Homo sapiens.

XX WO200212285-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US025269.

XX 10-AUG-2000; 2000US-0225033P.

PR 23-AUG-2000; 2000US-0227560P.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Killary A, Chandler D, Lott S;
XX WPI; 2002-269089/31.

DR New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.

XX Disclosure; Page 157-170; 185pp; English.

XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumor suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-lp36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene

XX Sequence 45845 BP; 12103 A; 10668 C; 10633 G; 12441 T; 0 U; 0 Other;

Query Match	26.08;	Score 995.8;	DB 6;	Length 45845;
Best Local Similarity	99.74;	Pred. No. 2.1e-180;		
Matches 1008;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;
Qy 1	AGGCTGCGCTGGACCGAAGCGGTGGCTTAAAGCTCGCGGGGTAAAGGGTTCGGCTGGG	60		
Db 24164	AGGCTGCGCTGGACCGAAGCGGTGGCTTAAAGCTCGCGGGGTAAAGGGTTCGGCTGGG	24223		
Qy 61	CAAGGGTTTGGGCGCGGATCCCGCAGCTGAGCGGGCGGCAACCCCTCTCTCTCTGCC	120		
Db 24224	CAAGGGTTTGGGCGCGGATCCCGCAGCTGAGCGGGCGGCAACCCCTCTCTCTCTGCC	24283		
Qy 121	GGTACAGCAATGTACGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG	180		
Db 24284	GGTACAGCAATGTACGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG	24343		
Qy 181	GCTTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT	240		
Db 24344	GCTTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT	24403		
Qy 241	CCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT	300		
Db 24404	CCGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCT	24463		
Qy 301	CCTCCCGCTCAGGATCTCGCTCCCTCAGCGCTCAGCGCTCAGCGCTCAGCGCTCAG	360		
Db 24464	CCTCCCGCTCAGGATCTCGCTCCCTCAGCGCTCAGCGCTCAGCGCTCAGCGCTCAG	24523		
Qy 361	TTGAGTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG	420		
Db 24524	TTGAGTCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG	24583		
Qy 421	GCGCACCCCTTCTCGGCTTACCCCTTCTCGGACAGCACCCCTTCTCGGCTTAC	480		
Db 24584	GCGCACCCCTTCTCGGCTTACCCCTTCTCGGACAGCACCCCTTCTCGGCTTAC	24643		
Qy 481	TCCTACCCCTTCTCGGCTTACCCCTTCTCGGACAGCACCCCTTCTCGGCTTAC	540		
Db 24644	TCCTACCCCTTCTCGGCTTACCCCTTCTCGGACAGCACCCCTTCTCGGCTTAC	24703		
Qy 541	GCGCGCGCTTCTCGACCCCGCTTCTCGGCTTACCCCTTCTCGGCTTACCCCTTCT	600		
Db 24704	GCGCGCGCTTCTCGACCCCGCTTCTCGGCTTACCCCTTCTCGGCTTACCCCTTCT	24762		
Qy 601	GCCATGCGCTGACGCTCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660		
Db 24763	GCCATGCGCTGACGCTCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	24822		
Qy 661	GACCCGCTGAGCTTGGGCTCGGAGCAGCTTCTTCTGCGCGCTGCTGCTGCTGCTG	720		
Db 24823	GACCCGCTGAGCTTGGGCTCGGAGCAGCTTCTTCTGCGCGCTGCTGCTGCTGCTG	24882		
Qy 721	GTGCGGAGGAGGCGCAGGCGCGCGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGG	780		
Db 24883	GTGCGGAGGAGGCGCAGGCGCGCGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGG	24942		
Qy 781	CCGCGCTGCGCGCGCGCGCGCTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG	840		
Db 24943	CCGCGCTGCGCGCGCGCGCGCTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG	25002		
Qy 841	CTGGAGCCCATCTCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	900		
Db 25003	CTGGAGCCCATCTCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	25062		
Qy 901	AAGCTTCTTCTGCTCAGGACCGCGCGCGCTTCTCTGCTTCTTCTGCGAGCGCTG	960		
Db 25063	AAGCTTCTTCTGCTCAGGACCGCGCGCGCTTCTCTGCTTCTTCTGCGAGCGCTG	25122		
Qy 961	CACGAGCAGCATCAGGTCACCGGCTCAGGAGCGCGCTTCTGCGAGCGCTGCGAG	1011		
Db 25123	CACGAGCAGCATCAGGTCACCGGCTCAGGAGCGCGCTTCTGCGAGCGCTGCGAG	25173		

RESULT 14

ABK12807
ID ABK12807 standard; DNA; 49744 BP.XX AC ABK12807;
XX

DT 18-JUN-2002 (first entry)

XX Human tumour suppressor CAR-1, BAC clone 392H05 5' sequence.
DEXX Human; ds; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer; BAC;
KW bacteria artificial chromosome; chromosome 1p31-1p36.XX Homo sapiens.
OSXX WO200212285-A2.
PNXX 14-FEB-2002.
PDXX 09-AUG-2001; 2001WO-US025269.
XX PFXX 10-AUG-2000; 2000US-0225033P.
XX PRXX 23-AUG-2000; 2000US-0227560P.
XX PRXX (TEXA) UNIV TEXAS SYSTEM.
PAXX Killary A, Chandler D, Lott S;
PIXX WPI; 2002-269088/31.
XX DRXX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
PTXX Disclosure; Page 135-148; 185pp; English.
PSXX The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1, or by
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence is a BAC (bacterial
CC artificial chromosome) containing part of the CAR-1 gene
XX
SQ Sequence 49744 BP; 13221 A; 11528 C; 11423 G; 13572 T; 0 U; 0 Other;Query Match 21.9%; Score 838.6; DB 6; Length 49744;
Best Local Similarity 93.5%; Pred. No. 2.4e-150;
Matches 951; Conservative 0; Mismatches 59; Indels 7; Gaps 7;QY 1 AGGCTGCGGTGACGACGAGCGGTGGCTGTAGCTCGCGGGGTAGAGGGTCCGCTGGG 60
Db 34306 AGGCTGCGGTGACGACGAGCGGTGGCTGTAGCTCGCGGGGTAGAGGGTCCGCTGGG 34365
QY 61 CCAGGGTTTGGGGCGGGGATCCGGCAGCTGAGCGGCGCGGCACCCCTCTCTCTCTGTC 120
Db 34366 CCA-GGTTTGGGGCGGGGATCCGGCAGCTGAGCGGCGCGGCACCCCTCTCTCTGTC 34424
QY 121 GGTACAGCCAAATGTACGGCTCGGGCTGGCTGCCCTCCCGCAGGATTCCTCCATCCCCA 180
Db 34425 GGTACAGCCAAATGTACTGCTCGGCTGGCTGCCCTCCCGCAGGATTCCTCCATCCCCA 34484
QY 181 GCTTCTCGCCCTCCCGGACCGCCCGCCGCGGATTTGAGACCCCTTAAAGGGTCCAC 240
Db 34485 GGTCTTGGCCCTTCCCGGACCGCCCGCCGCGGATTTGAGACCCCTTAAAGGGTCCAC 34544
QY 241 CCGGCTCGGGATCCCTTCTCCAGCTCTATTCCTTAGGACTGCCCGCCGCTTAGAA 300
Db 34545 CCGGCTCGGGATTCCTTCTCCAGCTCTATTCCTTAGGACTGCCCGCCGCTTAGAA 34604
QY 301 CTTCCCTC-GTCAGATTCCTGTC-CCTAGCGCTGACA-GCCTCTCCAGCGCCATC 357
Db 34605 CTTCCCTCAGTTAGGATTCCTGTCCTCAGCGCTCATAGCTTCTTTCCAGCGCCATC 34664
QY 358 GCG-TTGAGCTGCCACCTACC-TCTAGACTGCCCTCCCGGCTGGGCTCCAGGGAGTCT 415
Db 34665 GCTTTGAGCTGCCCTTACCTTTTATTTGCTTCCCGGGCTGGCTTTCCATGATTTT 34724
QY 416 CAGCGCGCACCCCTTCTCGGTTTACCTTCCCGGACAGCACCCCTTCTCTTCGG 475
Db 34725 CAGCGCGCACCCCTTCTCGGTTTACCTTCTTCGGACAGCACCCCTTCTCTTCGG 34784
QY 476 GTAGTCTTACCCCTGCTGTGCGGGCTGTGTCGCGGCCAGGCTCGGTGCTGCTC 535
Db 34785 GTAGTCTTACCCCTGCTGTGCGGGCTGTGTCGCGGCCAGGCTCGGTGCTGCTC 34844
QY 536 CGACAGCGCGC-GCTCTCAGCGCCCTTCCCGCTCGGCGCCCTCTCTCTGCTGCT 594
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QY 715 CACTGGGTGCGGAGGAGCGCGGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 774
Db 35025 CACTGGGTGCGGAGGAGCGCGGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 35084
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Db 35085 GCGGAGCCCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 35144
QY 835 TTCCCGCTGAGCGCATCTCTCAACGCGCGCGCGCGGCGGCTGCGGCGGCGGCGG 894
Db 35145 TTCCCGCTGAGCGCATCTCTCAACGCGCGCGCGCGGCGGCTGCGGCGGCGGCGG 35204
QY 895 AAGGTCAAGCTTCTTGCTTCAAGGACCGCGGCTTCTCTGCTTCTTCTGCGAGCGCT 954

Db 35205 AAGTCAAGCTTTTGGCTCAGGACCGGCGCTTCTGCTTCTTTGGAGAGGCT 35264

QY 955 GCACTGCAGGAGCAGCATCAGGTTCACCGCATCGACGAGCCCTTCAGCAGGCTGCAG 1011

Db 35265 GCACTGCAGGAGCAGCATCAGGTTCACCGCATCGACGAGCCCTTCAGCAGGCTGCAG 35321

RESULT 15

AAH06784

ID AAH06784 standard; cDNA; 628 BP.

XX

AC AAH06784;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA clone (5'-primer) SEQ ID NO:3619.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR

PR 27-AUG-1999; 99JP-00300253.

PR

PR 11-JAN-2000; 2000JP-00118776.

PR

PR 02-MAY-2000; 2000JP-00183767.

PR

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ora T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PT

PT

PS Claim 1; SEQ ID NO 3619; 2537pp + Sequence Listing; English.

XX

XX

CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX

XX

Sequence 628 BP; 83 A; 269 C; 170 G; 103 T; 0 U; 3 Other;

Query Match 15.5%; Score 592.2; DB 4; Length 628;

Best Local Similarity 97.3%; Pred. No. 1.3e-103;

Matches 611; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Db 1 CCACTACCTCTAGACTGCCCCCTCCGGGCTGGCGTCCACGGAGTCTCAGCGCGCACCCC 60

QY 430 TTCCTCGCGTTACCTTCCCTCCGGGACAGACACCCCTCTTCCGGTACTCTCTACCCC 489

Db 61 TTCCTCGCGTTACCTTCCCTCCGGGACAGACACCCCTCTTCCGGTACTCTCTACCCC 120

QY 490 TGGCTGTGGGGCTCTGCTCCCCCGCGCCAGCCCTCGGTCTGCTCGACGACGCGCGC 549

Db 121 TGGCTGTGGGGCTCTGCTCCCCCGCGCCAGCCCTCGGTCTGCTCGACGACGCGCGC 180

QY 550 TCTCTCAGCGCGCCCCCTCGCGCCCCCTCTCTCTGCTGCCCCCTGCGCGCATGGCG 609

Db 181 TCTCTCAGCGCGCCCCCTCGCGCCCCCTCTCTCTGCTGCCCCCTGCGCGCATGGCG 240

QY 610 TGCAGCTCAAGACGAGCTGCTGTCTCCATCTGCTTGAAGCATCTACAGGACCCGGTG 669

Db 241 TGCAGCTCAAGACGAGCTGCTGTCTCCATCTGCTTGAAGCATCTACAGGACCCGGTG 300

QY 670 AGCTTGGGCTGCGAGCACTACTTTCGCCCGCTGTCATCAGGAGCACTGGGTGCGGAG 729

Db 301 AGCTTGGGCTGCGAGCACTACTTTCGCCCGCTGTCATCAGGAGCACTGGGTGCGGAG 360

QY 730 GAGCGGAGGCGCGCGCACTGCCCCGAGTGGCGGGGACGCTTCGCCGAGCCCGCGCTG 789

Db 361 GAGCGGAGGCGCGCGCACTGCCCCGAGTGGCGGGGACGCTTCGCCGAGCCCGCGCTG 420

QY 790 GCGCCAGCCCTCAAGCTGGGCAACATCGTGAGCGCTTCTTCCCGCTGCAAGCC 849

Db 421 GCGCCAGCCCTCAAGCTGGGCAACATCGTGAGCGCTTCTTCCCGCTGCAAGCC 480

QY 850 ATCTCAACG 909

Db 481 ATCTCAACG 540

QY 910 TGGCTCAAGACGCGCGCGCTTCTGCTTCTTCTGCGAGC-AGCTGCACTGCAAGCA 968

Db 541 CTGCTCAAGACGCGCGCGCTTCTGCTTCTTCTGCGAGCAAGCTGCACTGCAAGCA 600

QY 969 GCATCAGTCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCT 996

Db 601 GCATCAGTCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCTGCAAGGCT 628

Search completed: July 31, 2004, 12:54:57

Job time : 1378 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	2322.2	60.7	23433	9	US-09-927-091-7	Sequence 7, Appli
3	2308.6	60.3	30676	9	US-09-927-091-8	Sequence 8, Appli
4	2252.8	58.9	30625	9	US-09-927-091-5	Sequence 5, Appli
5	995.8	26.0	45845	9	US-09-927-091-6	Sequence 6, Appli
6	838.6	21.9	47474	4	US-09-927-091-4	Sequence 4, Appli
C 7	609.6	15.9	610	13	US-10-027-632-100265	Sequence 100265,
C 8	609.6	15.9	610	16	US-10-027-632-100265	Sequence 100265,
C 9	562	14.7	573	9	US-09-864-761-7231	Sequence 7231, Ap
C 10	431	11.3	431	9	US-09-864-761-23962	Sequence 23962, A
C 11	160.2	4.2	2045	16	US-10-094-749-1459	Sequence 1459, Ap
12	136.4	3.6	1394	9	US-09-764-868-418	Sequence 418, App
13	132.4	3.5	3038	16	US-10-102-980-277	Sequence 277, App
14	122.8	3.2	1904	16	US-10-104-047-103	Sequence 103, App

Db	121	GGTCAAGCAATGTACGGCTCGCGCTGGCTGCCCTCCCGCAGGATTCGCCATCCCA	180	1201	CTGAGGCGGACACGGCCCGCAGCGCTGACGACATCGAGCAAGTCCAGCGCTACAGC	1260
Qy	181	GCTTCTCGCCCTCCCGACCGCCCGCCACCCCGGATTTGACCCCTTTAAGGGCTCCAC	240	1261	CAGAGTGCACAAAGTTCAGGAGGGAGCCAGATCTCTGAGGAGCGCTGGCTGAAACC	1320
Db	181	GCTTCTCGCCCTCCCGACCGCCCGCCACCCCGGATTTGACCCCTTTAAGGGCTCCAC	240	1261	CAGAGTGCACAAAGTTCAGGAGGGAGCCAGATCTCTGAGGAGCGCTGGCTGAAACC	1320
Qy	241	CCCGCTCGGGATCCCTTCTCCAGCTCTATCCCTTAGGACTGCCCGCCCTTAGAA	300	1321	GACCGGACACCTTCTTGCTGGGTGGCTCTCACTGTCGAGCGGCTCAAGGGAAAAATC	1380
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Qy	301	CCTCCCTCAGAGTCTCGCTCCCTCAGCGCTCAGCGCTCTCCAGCGCCATCGCC	360	1381	CATGAGACCAACCTCACATATGAAGCTTCGAGCTCCAGATCACAGGCCCTTGAG	1440
Db	301	CCTCCCTCAGAGTCTCGCTCCCTCAGCGCTCAGCGCTCTCCAGCGCCATCGCC	360	1381	CATGAGACCAACCTCACATATGAAGCTTCGAGCTCCAGATCACAGGCCCTTGAG	1440
Qy	361	TTGAGCTGCCACTACCTAGCTAGCTCCCTCCCGGCTGGCTCCAGCGAGTCTCAGCC	420	1441	TACACCATCTGGAAGTCCCTGTTCCAGACATCCACCCAGTCCGAGCGCCCTTAACCTG	1500
Db	361	TTGAGCTGCCACTACCTAGCTAGCTCCCTCCCGGCTGGCTCCAGCGAGTCTCAGCC	420	1441	TACACCATCTGGAAGTCCCTGTTCCAGACATCCACCCAGTCCGAGCGCCCTTAACCTG	1500
Qy	421	GCGCAACCCCTTCTCGCGCTTACCTCTTCGGAACAGCAACCCCTCTCTTCGCGTAGC	480	1501	GACCGGACACAGCCACAGCGCTGATCTCTGTCGAGCACTGACCACTTGTGGCTTAC	1560
Db	421	GCGCAACCCCTTCTCGCGCTTACCTCTTCGGAACAGCAACCCCTCTCTTCGCGTAGC	480	1501	GACCGGACACAGCCACAGCGCTGATCTCTGTCGAGCACTGACCACTTGTGGCTTAC	1560
Qy	481	TCCTACCCCTGCTGTGGGCTCGTCCCGGCGCCAGCCCTCGGTGCTGCTCCGACA	540	1561	GGCAACTTGGACCCACAGCACTGAGGACTGCGCAAGCGCTTCGATGTGAGGTGTG	1620
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Qy	541	GCGCGCGCTCTCTCAGCGCGCCCTGCTCCCTCGCGGCCCTCTCTGCTGCCCTGGC	600	1621	GTGCTGGGTCTGAAGCTTCACTAGTAGTGGCGTCCACTACTGGAGGTGGTGGCGGAG	1680
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Qy	601	GCCATGGGCTGAGGCTCAAGGACAGCTGTGCTGCTCCATCTGCTGAGCATCTACAG	660	1681	AAGACCCAGTGGGTGATCGGGCTGGCACACGAAGCGCGCAAGCGGACAGTCCAG	1740
Db	601	GCCATGGGCTGAGGCTCAAGGACAGCTGTGCTGCTCCATCTGCTGAGCATCTACAG	660	1681	AAGACCCAGTGGGTGATCGGGCTGGCACACGAAGCGCGCAAGCGGACAGTCCAG	1740
Qy	661	GACCGGTGAGCTGGGCTGCGAGCACTACTTCTGCGCGCTGCTATCAGGAGCACTG	720	1741	ATCCAGCCAGCGCGGCTTCTACTGCTGATGATGATGATGATGATGATGATGATGATG	1800
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Qy	721	GTGCGGAGAGGCGGAGGCGCGCGCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCG	780	1801	TGCAAGGAGCGCGGCTTACGCTCGCGGCAAGCTTACAAAGGTGGGTGCTTCTC	1860
Db	721	GTGCGGAGAGGCGGAGGCGCGCGCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCG	780	1801	TGCAAGGAGCGCGGCTTACGCTCGCGGCAAGCTTACAAAGGTGGGTGCTTCTC	1860
Qy	781	CCCGGCTGCGGCTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT	840	1861	CTGGACTATGACCAAGGCTTGTCTTCTCAATGCTGATGATGATGATGATGATGATG	1920
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Qy	1021	AAGGACCACTTCAAGCGCGCTTCAAGACAGGAGCGGAAACACCGAGCGCTG	1080	2101	AAGACCTGAGCTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAGTGTGTTTACCTCC	2160
Db	1021	AAGGACCACTTCAAGCGCGCTTCAAGACAGGAGCGGAAACACCGAGCGCTG	1080	2101	AAGACCTGAGCTCCAGCCACCGTGGCCACTGAGACCTCAGGCGAGTGTGTTTACCTCC	2160
Qy	1081	CTCAAGCGACAACTGGCGGAGCAAGTCTTCAACAGAGCTTGGGACCACTATCGGC	1140	2161	AGCTCCAGTCTGTAAATGGAGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2220
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Qy	1141	GAGGCTTCAAGCGGCTGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200	2221	GATGTTCTGAGCTCTGACCTTGTATGGGATACAGCTTGTATCAAGGATGTGATGGC	2280
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RESULT 2

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US-09-927-091-7
; Sequence 7, Application US/09927091
; Patent No. US2020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: US/09927091
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 23433
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (5071)..(23433)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-7
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Query Match 60.7%; Score 2322.2; DB 9; Length 23433;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2350; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

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QY	1609	GTGAGGTGTCGGTCTGGGTCTTGAAGCCCTTCACTAGTGGCTCCACTACTCTGGAGGTG	1668	Db	13739	TGCCACAGGCCGAGGACAGGGTATATCCCAAAGCTGATGACAGCCCATTAGC	13798
Db	12660	GTGAGGTGTCGGTCTGGGTCTTGAAGCCCTTCACTAGTGGCTCCACTACTCTGGAGGTG	12719	QY	2749	CTAAAGCAACTGAGGACAGCCCTCCCTGATGATCGAGGTCCCACTAGCTCTGAACA	2808
QY	1669	GTGTGGCGGAGAAAGCCACGTGGGTGATCGGGCTGGCACAGAGCGCAAGCGCAAG	1728	Db	13799	CTAAAGCAACTGAGGACAGCCCTCCCTGATGATCGAGGTCCCACTAGCTCTGAACA	13858
Db	12720	GTGTGGCGGAGAAAGCCACGTGGGTGATCGGGCTGGCACAGAGCGCAAGCGCAAG	12779	QY	2809	AGAGTCCAGCAACCCCTCTTCAGCCAGGCCCTCTGTGACCTGTGAGGTGTCAGGAGGCTTC	2868
QY	1729	GGCAGATCCAGATCCAGCCAGCCGCGGCTTCTACTGCATCGTGAATGACAGATGGCAAC	1788	Db	13859	AGAGTCCAGCAACCCCTCTTCAGCCAGGCCCTCTGTGACCTGTGAGGTGTCAGGAGGCTTC	13918
Db	12780	GGCAGATCCAGATCCAGCCAGCCGCGGCTTCTACTGCATCGTGAATGACAGATGGCAAC	12839	QY	2869	CAGAAGCAGTGTGTTTAATTAGGACCCAAAGCACTGGGAGGGGCTGTTGGCTAGACCCCTT	2928
QY	1789	CAGTACAGCGCTGCAACGAGCCCTGGACGGGCTTAAGCTCCGGGACAAAGCTTGCACAG	1848	Db	13919	CAGAAGCAGTGTGTTTAATTAGGACCCAAAGCACTGGGAGGGGCTGTTGGCTAGACCCCTT	13978
Db	12840	CAGTACAGCGCTGCAACGAGCCCTGGACGGGCTTAAGCTCCGGGACAAAGCTTGCACAG	12899	QY	2929	GTGACACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAAACAAGGCCACTTTGTAG	2988
QY	1849	GTGGGTGTCCTTGGATGATGACCAAGCTTGTCTCATCTCAATGCTGATGACATG	1908	Db	13979	GTGACACTTGGCATCTATCTCAGTTAGGATCCTGCTGCAGAAAAACAAGGCCACTTTGTAG	14038
Db	12900	GTGGGTGTCCTTGGATGATGACCAAGCTTGTCTCATCTCAATGCTGATGACATG	12959	QY	2989	CTGGTTTAAATAGACAAGGATTTACTACTGGCCCTCTGTGGCTTGCAAAATTTGTGGAA	3048
QY	1909	TCTTGGCTCTACACCTTCGCGAGAGATTCCCTGGCAAGCTCTGCTTTACTTTGAGCCCT	1968	Db	14039	CTGGTTTAAATAGACAAGGATTTACTACTGGCCCTCTGTGGCTTGCAAAATTTGTGGAA	14098
Db	12960	TCTTGGCTCTACACCTTCGCGAGAGATTCCCTGGCAAGCTCTGCTTTACTTTGAGCCCT	13019	QY	3049	GAGCTGGAGAAAGCAGCTCTGCTGATTTTCCAGGAACCTCCAGCGCCAGATTCATCATGT	3108
QY	1969	GGCCAGAGCCAGCCATGGCAAGAACGTTGAGCGCTGCGGATCAACACCGTCCGCAATC	2028	Db	14099	GAGCTGGAGAAAGCAGCTCTGCTGATTTTCCAGGAACCTCCAGCGCCAGATTCATCATGT	14158
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QY	2029	TAGTCCAGCAGAGGAGACCAACCTCTCTGGACCACTGCCACTGCAAGAGCCCTGC	2088	Db	14159	CTGTTGTGACCAAGGAAGCTGCCCATCTGCGAGGAAGCCACTATGCCAGAAAGCTGCTG	14218
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QY	2089	CCAGGAAGATAGAAGACCTTGAATCCAGCCCAACCGTGGCCACTGGAGACTCAGGCCAGT	2148	Db	14219	ACTGCAGAACTAGGCTCCCTCTGCGACCGTCCGTCGACCCCAATAGATGCTCTGAGCCCT	14278
Db	13140	CCAGG-AGATAGAGACCTTGAATCCAGCCCAACCGTGGCCACTGGAGACTCAGGCCAGT	13198	QY	3229	GCCCTCTCCCACTTCACTAGTCTCCAAATCTAAATTTTACAAGAGATTCCTGTTGGG	3288
QY	2149	TGTTTACCTCCAGCTCAGTCTGTAAATGGAGTTGCATTCCTTCTTCTTAACTC	2208	Db	14279	GCCCTCTCCCACTTCACTAGTCTCCAAATCTAAATTTTACAAGAGATTCCTGTTGGG	14338
Db	13199	TGTTTACCTCCAGCTCAGTCTGTAAATGGAGTTGCATTCCTTCTTCTTAACTC	13258	QY	3289	GGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAATGTCATTTCCCT	3348
QY	2209	TCTTCCAGCATCGATGCTGTAGCTCTGACCTTGTATGGGATACAGCTTTGATCCAAG	2268	Db	14339	GGAACTTAAGTCAGATCCAGAACCTTGGCTGCAAGGGAGTCTGGGAAATGTCATTTCCCT	14398
Db	13259	TCTTCCAGCATCGATGCTGTAGCTCTGACCTTGTATGGGATACAGCTTTGATCCAAG	13318	QY	3349	AGAAGCAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTTCTGCCACAGATCCAA	3408
QY	2269	ATGTGACATGGCTTCTCCTCAGGCAACCCCTGCCCAACCCCTCATCCCCATCTTCAGG	2328	Db	14399	AGAAGCAAGTTAGGGTGGGTGGAGCAAGCCCACTGCGTTTTTCTGCCACAGATCCAA	14458
Db	13319	ATGTGACATGGCTTCTCCTCAGGCAACCCCTGCCCAACCCCTCATCCCCATCTTCAGG	13378	QY	3409	TCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTTGCTGCCCCCTTGGCTCT	3468
QY	2329	GGCAGGGGATACCTTCCAGTGTCTCCCTCAGCCAGCCCTGACCTCAGGAAGTGTGAG	2388	Db	14459	TCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTAGGGTTGCTGCCCCCTTGGCTCT	14518
Db	13379	GGCAGGGGATACCTTCCAGTGTCTCCCTCAGCCAGCCCTGACCTCAGGAAGTGTGAG	13438	QY	3469	ATCCCTGCCAGAGGTGGGAACCTGGAGAGTGGCTGCAAGACTGAGCCCTTAAATGCTCC	3528
QY	2389	AGCATGCCAGTAGTTGGAGCCCGAAGACACACAGACCCCTTATGTCCTTATGCTCCATG	2448	Db	14519	ATCCCTGCCAGAGGTGGGAACCTGGAGAGTGGCTGCAAGACTGAGCCCTTAAATGCTCC	14578
Db	13439	AGCATGCCAGTAGTTGGAGCCCGAAGACACACAGACCCCTTATGTCCTTATGCTCCATG	13498	QY	3529	CCGGCTTGAATTTCTTTCTAGTCTGCGGCTTAGATTCGACATCTGCGGCTCTCTGACA	3588
QY	2449	AAGACTTACCCCTGACCAAGCTAGTGAAGGCAATTTACCTTGAACCCAGTCCACAGTG	2508	Db	14579	CCGGCTTGAATTTCTTTCTAGTCTGCGGCTTAGATTCGACATCTGCGGCTCTCTGACA	14638
Db	13499	AAGACTTACCCCTGACCAAGCTAGTGAAGGCAATTTACCTTGAACCCAGTCCACAGTG	13558	QY	3589	CAACACACCATCCCAAGTAGCCGGAAGCTTAAACACAGGGGCTTCTTAAATGGCTGC	3648
QY	2509	GTACAGGTAGTACCTGGTCTAGGTTGCTGAGAGCAACCTCTCTGCAACCCCTCCAC	2568	Db	14639	CAACACACCATCCCAAGTAGCCGGAAGCTTAAACACAGGGGCTTCTTAAATGGCTGC	14698
Db	13559	GTACAGGTAGTACCTGGTCTAGGTTGCTGAGAGCAACCTCTCTGCAACCCCTCCAC	13618	QY	3649	CCCCGCCACCGGCGCTCCCTTGGGCAAAAGGAATTTGTGAGCCCTACCCCAACCCCTCAA	3708
QY	2569	ACCAAGAACTATATGTTTCTTCTTCTTCCATGATCTGCTGGTCAAGTATGATGCTGTG	2628	Db	14699	CCCCGCCACCGGCGCTCCCTTGGGCAAAAGGAATTTGTGAGCCCTACCCCAACCCCTCAA	14758
Db	13619	ACCAAGAACTATATGTTTCTTCTTCTTCCATGATCTGCTGGTCAAGTATGATGCTGTG	13678	QY	3709	CTACCAAGATCTGGGCCAACCCAGCAGTATTTTATTTAAATGTTGCCCACTTTATGAG	3768
QY	2629	GCTGTGGAAGGACCTGTGATGTTGATCCACATTAATGATGTCGACCACTTCC	2688	Db	14759	CTACCAAGATCTGGGCCAACCCAGCAGTATTTTATTTAAATGTTGCCCACTTTATGAG	14818
Db	13679	GCTGTGGAAGGACCTGTGATGTTGATCCACATTAATGATGTCGACCACTTCC	13738	QY	3769	TTATGATCAATTTGATTAATTAAGTTACAGATGCA	3807
QY	2689	TGCCACAGGCCGAGGACAGGGTATATCCCAAAGCTGATGACAGGCCCATTAGC	2748				

Db 14819 TTATGATCAATTTGTATTAATTAAGTTACAGATGTCA 14857

RESULT 3

US-09-927-091-8

; Sequence 8, Application US/09927091

; Patent No. US20020119541A1

; GENERAL INFORMATION:

; APPLICANT: KILLARY, ANN

; APPLICANT: LOTT, STEVE

; APPLICANT: CHANDLER, DAWN

; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1

; FILE REFERENCE: UTSC:651US

; CURRENT APPLICATION NUMBER: US/09/927,091

; CURRENT FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/227,560

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: 60/225,033

; PRIOR FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 30676

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: modified base

; LOCATION: (6671)..(30676)

; OTHER INFORMATION: n = A or C or G or T/U

US-09-927-091-8

Query Match 60.3%; Score 2308.6; DB 9; Length 30676;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 2348; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

QY 1429 GGGCCCTGAGTACACATCTGGAATGCCCTTCCAGGACATCCACCCAGTGCACGCC 1488

Db 23371 GGTCCACAGCGCTTCTCCCACTCATCTCTCCCTCTCCACCCCAAGTGCACGCC 23430

QY 1489 GCCTTAACCTGGACCCGGGACAGCCACAGCGCTGATCTCTGTCGGAGCATGCAC 1548

Db 23431 GCCTTAACCTGGACCCGGGACAGCCACAGCGCTGATCTCTGTCGGAGCATGCAC 23490

QY 1549 ATTGTGGCTTACGGCACTTGCACTCCACAGCCACTGCAGGACTCGCCAAAGCGCTTCGAT 1608

Db 23491 ATTGTGGCTTACGGCACTTGCACTCCACAGCCACTGCAGGACTCGCCAAAGCGCTTCGAT 23550

QY 1609 GTGGAGTGTGGTGTGGTGTCTGAAGCCTTCAGTAGTGGCGTCCACTACTGGAGGTG 1668

Db 23551 GTGGAGTGTGGTGTGGTGTCTGAAGCCTTCAGTAGTGGCGTCCACTACTGGAGGTG 23610

QY 1669 GTGGTGGCGGAGAGACCCAGTGGGTGATCGGGCTGGACAGGACTCGCCAAAGCGCCGCAAG 1728

Db 23611 GTGGTGGCGGAGAGACCCAGTGGGTGATCGGGCTGGACAGGACTCGCCAAAGCGCCGCAAG 23669

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QY 1789 CAGTACAGCGCTGACGGAGCCCTGGACGCGGCTTAACTGCGGACAGCTTGAACAG 1848

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Db 23850 TCTGGCTCTACACCTTCGCGAGAGTTCCTCTGCAAGTCTGCTTCTACTTCACTTCACTGACCCCT 23909

QY 1969 GGCAGAGCCAGCCAAATGGCAAGACGTTACGCGCTGCGGATCAACACCGTCCGCATC 2028

Db 24989 GAGCTGGAGAGCAGACTCTGTGATTTCCAGGAACTCCAGCGCCAGATTCTATCTGT 25048

Db 23910 GGCAGAGCCAGCCAAATGGCAAGACGTTACGCGCTGCGGATCAACACCGTCCGCATC 23969

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Db 24989 GAGCTGGAGAGCAGACTCTGCTGAATTTCCAGGAACTCCAGCGCCAGATTCTATCTGT 25048

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QY 3109 CTCTGTGTGACACAGAAAGCTGCCCCCATCTGCGAGAAAGCCACTATGCGAGAAAGCTGCTG 3168
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QY 3169 ACTGACAGACTAGGCTCCCTCTGCGACGCTCCGTCGCGAGCAATAGATGCTCCTGAGGCT 3228
Db 25109 ACTGACAGACTAGGCTCCCTCTGCGACGCTCCGTCGCGAGCAATAGATGCTCCTGAGGCT 25168
QY 3229 GCGCCTCTCCACATCTCACTAGTTCCCAAAATCTAAATTTTACAGAGATTTCTGTTGGG 3288
Db 25169 GCGCCTCTCCACATCTCACTAGTTCCCAAAATCTAAATTTTACAGAGATTTCTGTTGGG 25228
QY 3289 GGAATCTTAAGTCAGATCCAGAACCTTGCTGCGAAGGAGTGTGGGAATGATTTCCCT 3348
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RESULT 4
US-09-927-091-5
; Sequence 5, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 30625
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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; NAME/KEY: modified base
; LOCATION: (4754)..(30625)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-5

Query Match 58.9%; Score 2252.8; DB 9; Length 30625;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 57; Indels 3; Gaps 3;

QY 1429 GGCCCCCTGCGAGTACACATCTGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCC 1488
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Db 22206 GGCAGATCCAGATCCAGCCACAGCCGCGGCTTCTACTGATCTGATGACGATGGCAC 22265
QY 1789 CAGTACAGCGCTGACAGCGCCCTGGACGGCTTAACTCCGGGACAAAGCTTGCACAG 1848
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Db 22386 TCCTGGCTTACACCTTCCTCGGAGAAATTCCTGCGAGAAATTCCTGCGAGAAATTCCTGCGAG 22445
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Db 22446 GGCAGAGCCACGCCAATGGCAAGAAAGCTTTCAGCGCTGCGGATCAACACCGCTCCGCATC 22505
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US-10-027-632-100265/c
; Sequence 100265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100265
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-100265

Query Match 15.9%; Score 609.6; DB 13; Length 610;
Best Local Similarity 99.8%; Pred. No. 6.9e-160;
Matches 609; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY	2405	GGCAGCCCGAAAGCACACAGCACCTCTTATGTCCCATGCCCTTAAGCTTACCCTGCAC	2464
Db	550	GGCAGCCCGAAAGCACACAGCACCTCTTATGTCCCATGCCCTTAAGCTTACCCTGCAC	491
QY	2465	CAAGCTAGTATGGGCCATTATACCCTTTGACCCCAAGTCCACAGTGGTCCAGGTTAGTACCT	2524
Db	490	CAAGCTAGTATGGGCCATTATACCCTTTGACCCCAAGTCCACAGTGGTCCAGGTTAGTACCT	431
QY	2525	GGTCTTAGGTTGGCTGAGAGCCAACTCTCTCTGCCACCCCAACCAAGAACTATATGG	2584
Db	430	GGTCTTAGGTTGGCTGAGAGCCAACTCTCTCTGCCACCCCAACCAAGAACTATATGG	371
QY	2585	TTCCTACTTCTCCACATGATCTGTGGTCAAGTATGCTGTGGCTGTGGAGGCACC	2644
Db	370	TTCCTACTTCTCCACATGATCTGTGGTCAAGTATGCTGTGGCTGTGGAGGCACC	311
QY	2645	TGTTAGTTAGTCCACATTTATAGTCCACCACTTCTCTGCCACAGGCGGAGG	2704
Db	310	TGTTAGTTAGTCCACATTTATAGTCAATGTGCCAACCTTCTGCCACAGGCGGAGG	251
QY	2705	GACAGGTGAGGTATACCAAAGTGTATGACAGAGCCCAATAGCTTAAAAGCAACTGCAG	2764
Db	250	GACAGGTGAGGTATACCAAAGTGTATGACAGAGCCCAATAGCTTAAAAGCAACTGCAG	191
QY	2765	GACAAGCCTCCCTGGATGATCGAGGTCCCCAGTAGCTCTGAACAAGAGTCCAGCCAACC	2824
Db	190	GACAAGCCTCCCTGGATGATCGAGGTCCCCAGTAGCTCTGAACAAGAGTCCAGCCAACC	131
QY	2825	TCTTCAGCCAGGCTCTGTGACCTGTAGGGTCCAGAGGCTTCCAGAGCAAGTGTGTTGT	2884
Db	130	TCTTCAGCCAGGCTCTGTGACCTGTAGGGTCCAGAGGCTTCCAGAGCAAGTGTGTTGT	71
QY	2885	AATTAGGACCAAGCACTGGAGGGGCTGTGGCTAGACCCCTTGTTCAGACTTGGCATCT	2944


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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 43117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 23962
; LENGTH: 431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC02262.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; OTHER INFORMATION: EST HUMAN HIT: BE315402.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q02084, EVALUE 5.00e-28
; OTHER INFORMATION: NT HIT: g111423970, EVALUE 0.00e+00
US-09-864-761-23962

Query Match 11.3%; Score 431; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.6e-110;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1643 GTACTGGGGTCCACTACTCGGAGGTGGTGGTGGGAGAGACCCAGTGGGTGATCGGGC 1702
DB 431 GTAGTGGGCTCCACTACTCGGAGGTGGTGGTGGGAGAGACCCAGTGGGTGATCGGGC 372
QY 1703 TGGCACACGAAGCCGCAAGCCGAGGAGGATCCAGATCCAGTCCAGCCCGCGGCTTCT 1762
DB 371 TGGCACACGAAGCCGCAAGCCGAGGAGGATCCAGATCCAGTCCAGCCCGCGGCTTCT 312
QY 1763 ACTGATCGTGTATGCACGATGGCAACAGTACAGCGCTGCAAGGAGCCCTCGAGCGGC 1822
DB 311 ACTGATCGTGTATGCACGATGGCAACAGTACAGCGCTGCAAGGAGCCCTCGAGCGGC 252
QY 1823 TTAAGCTCCGGACAGCTTGACAGGTGGGTGTCTTCTGACTATGACCAAGGCTTGC 1882

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DB 251 TTAAGCTCCGGACAGCTTGACAAAGTGGGTGTCTTCTCGACTATGACCAAGGCTTGC 192
QY 1883 TCATCTTTTACAATGCTGATGACATGTCCTGGCTCTTACACCTTCGCGAGAAAGTTCCCTG 1942
DB 191 TCATCTTTTACAATGCTGATGACATGTCCTGGCTCTTACACCTTCGCGAGAAAGTTCCCTG 132
QY 1943 GCAAGCTCTGCTCTTACTTACGCCCTGGCAGAGCCGCAATGGCAAGACGTTCCAGC 2002
DB 131 GCAAGCTCTGCTCTTACTTACGCCCTGGCAGAGCCGCAATGGCAAGACGTTCCAGC 72
QY 2003 CGCTGGCGATCAACACCGTCCGCACTAGTCCAGGAGAGGAGACCAACACCTTCTGGG 2062
DB 71 CGCTGGCGATCAACACCGTCCGCACTAGTCCAGGAGAGGAGACCAACACCTTCTGGG 12
QY 2063 ACCACTGCCAC 2073
DB 11 ACCACTGCCAC 1

RESULT 11
US-10-094-749-1459
; Sequence 1459, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-03-12
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1459
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1459

Query Match 4.2%; Score 160.2; DB 16; Length 2045;
Best Local Similarity 48.9%; Pred. No. 1.3e-33;
Matches 663; Conservative 0; Mismatches 648; Indels 44; Gaps 7;

QY 616 CTCAGGAGAGCTGCTGTGCTTCCATCTGCTTACGATCTACAGGACCCGCTGAGCCTG 675
DB 229 CTGGAGGACCGGCTTCAGTGTCCCATCTGCTTGGAGGCTTCAAGAGAGCCCTGATGCTG 288
QY 676 GCGTCGGAGCACTACTTCTGCGCGCTGTCATCAGGAGCACTGGTGGCGGAGGAGCG 735
DB 289 CAGTGTGGCCACTCTTACTTGCAGGGGCTGCTGTTCCTCTGCTGCACCTGGATGCC 348
QY 736 CAGGCGCGCCGCACTGCGCCGAGTGGCGGCGACGTTCCGCGAGCCCGCGCTGGCGCCC 795
DB 349 GAG-----CTGCGCTGCCCGCTGTGCGCGCAGGCGGTGGATGGCAGCAGCTCCCTGCC 402

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Qy	796	AGCCTCAAGCTGGC	AAACATCGTGAGCGCTACAGCTCCTTCCCGCTGGAGCCATCTCTC	855
Db	403	AACGTCTCCCTGGCC	AGGGTGATCGAAGCCCTTAGG--CTCCTTGGGGAGCCCGAGCCCA	460
Qy	856	AACGGCGCGCGCG	CGCGACCTCTCCAGGGGACGACAAGGTCAAGCTCTTCTTGGCTC	915
Db	461	AGTCTGCGTGAC	ACCGGAACCGC-----TCAGCCTTTCTGCGAG	504
Qy	916	ACGGACCGCGCTT	CTCTGCTTTCTGCGACGACCTGCTACGACGAGCATCAG	975
Db	505	AAGGACGAGGCT	CTCTCTGGGCTCTGGGCTCCACCAACACCAACCG	564
Qy	976	GTCAACGGCATCA	GACGAGCTTCGACGAGCTCCAGAGGAGCTGAAGCAACCACTTCAG	1035
Db	565	GTACGCGCGCTTC	ACCGCTTACGCGCATGAAGAGAGCTCGACGCTCTCTCT	624
Qy	1036	GCCCTTCAAGAC	AGCGAGCAACACGAAAGCTGCGTGTCTAAGCGCAACTCTG	1095
Db	625	GAGCTGAAGCAG	GAGAGAAAAAGGTGATGAGCTCATCGCCTGCTGTAACACCG	684
Qy	1096	GCGAGACCAAGT	CTTCCACAAAGAGCTCGGACCACTATCGCGAGGCTTCGAGCG	1155
Db	685	ACCCGAATCTCA	TGAGTCCGATGTTTCTGAGTCTCGCGCGAGTTCCAGGAG	744
Qy	1156	CTGCACCGGTCT	CGCTGAAACGCAAGGCCATGCTAGAGGAGCTGGAGCGGACACG	1215
Db	745	CTGCACCACTG	TGATGAGGAAAGCCCGCTGCTGGAGGGAT--AGGGGGTCTAC	802
Qy	1216	GCCGCGAGCTGA	CCGACATCGAGCAAGAAAGTCCAGGCTTACAGCAGCAGCTGCCAAG	1275
Db	803	ACCCGTGGCTGT	GTGGCTCCTCTGGAATGAGTGAGAGCAGCGCCAGGGAACCCGGGAG	862
Qy	1276	GTCAGAGGGAG	CGCCAGATCTCGAGAGCGGTGCTGAAACCGACCGGACACCTTC	1335
Db	863	CGGCTGGCGCC	AGCCGAGTGTCTCGAACAGTTCGGCAATGAGGACCAACCAAGTTC	922
Qy	1336	CTGGCTGG-----	GGTGGCTCACTGTCCGAGCGGTCAAGGGAAAAATCCATAGAGCC	1389
Db	923	ATCCGGTTCAC	TCCATCCATGGCTTCCAGAGCAGAGATGCGCAGGCCCGGCCCTTTAGAGGC	982
Qy	1390	AACCTCAATAT	GAAAGACTTCCGACCTCCAAGTACACAGCCCTCGAGTACACCATC	1449
Db	983	GCATTCACCCCA	CTCTCTTCAAGCCAGGCTCCACCAAGGTGACATCAAGCTGACCGTG	1042
Qy	1450	TGGAAGTCCCTG	TTCAGGACATCAACCCAGTGCAGCCGCTTAACCTTGGACCCGGGC	1509
Db	1043	TGGAAGGCTCT	TCGGAAGTTTTCGACCCCGGAGCTCTCAAGTTGGACCTCGCC	1102
Qy	1510	ACAGCCCAACG	CGCTGATCTCTFPGAAGACTGACCAATGTGGCTTACGGCACTTG	1569
Db	1103	ACTGCCCAACCA	CTCTCTGGAGCTCTC---CAAGGGCAACAGGTGTGTCAGTGGGGCTT	1159
Qy	1570	CACCCAGAGCCA	CTGCAGCTCCCAAGCGCTTCGATGTGGAGGTGTGGGTCTGGGT	1629
Db	1160	CTGGCCACGCG	CGAGCAGCGCTGAGCGCTTCGATACAGCACTTGGCTCTGGCC	1219
Qy	1630	TCTGAAGCCTT	CAGTAGTGGGCTCCACTCTGGAGGTGTGTGGCGGAGAGACCCAG	1689
Db	1220	AGCCCGGCTT	CTCTCGCGCGCACTTCTGGAGGTGTGTGGCGGACGACGAGCGAC	1279
Qy	1690	TGGGTGATCGG	CTGGACAGAGCCGACAGAGCCGAGGCGACATCCAGATCCAGCCC	1749
Db	1280	TGGCGCTTGG	GGTTCATCAAGGGGACAGCCAGCGCTTAAGGGCAAGCTGAACAGTCTCCC	1339
Qy	1750	AGCCCGGCTT	CTACTGTCATCGTATGACGATGGCAACCAAGTACAGCGCTTCACGGAG	1809
Db	1340	GAGCACGCGGT	GTGCTGATCGGCTTGAAGGGGCGCGGTGTACGAAGCCTTTTGCCTGC	1399
Qy	1810	CCCTGGAACG	CGGCTTAAAGTTCGCGGACAAAGCTTGAACAGTGGGTGTCTTCTGACTAT	1869
Db	1400	CCCGGGTACCC	CTCCGCTGGCGGACCCCAACCGCATCGGGCTCTATGCACTAT	1459

Qy	1870	GACCAAGGCTTGCTCATCTCTCTCAATG-----CTGATGACATGTCCTGGCTCTAC	192
Db	1460	GAGCAGGGCGAACTACACTTCTTCGATGCGGACGGCCCCGATGCTGGCGGCTCTAC	1519
Qy	1921	ACCTTCGGCGAGAAAGTTCCCTGGCAAGCTCTGTC	1955
Db	1520	ACCTTCAGCGCCGCACTTCCAGGGCAAGCTGTACCC	1554

RESULT 12

```

RESULT 12
US-09-764-868-419
; Sequence 418, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764.868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 418
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-418

```

Query Match	3.6%;	Score 136.4;	DB 9;	Length 1394;
Best Local Similarity	54.9%;	Pred. No. 4.9e-27;		
Matches 269; Conservative	0;	Mismatches 221;	Indels 0;	Gaps 0;

1482	QY	GCACGCCGCCCTAACTCTGGACCGGGCACAGCCACACAGCGCTGATCTCTGTGGACGA	150
45	Db	GCCAGCGGATGTGACCTCTGGACCGCTGACAGAGCTCATCTTAACCTAGTCTCTGTGACAGGA	104
1542	QY	CTGCACCATTCTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAAAGCG	1601
105	Db	TCGTAAGAGCGTCAAGTTTCGTGGAGACAAGACTCCGGGATCTCCCTGACACACCAAGGCG	164
1602	QY	CTTCGATGTGAGAGTGTCGGTGTCTGGGTCTTGAAGCTTTCAGTAGTGGCGTCCACTACTG	166
165	Db	TTTCACTCTTCACTCCCTTCGCTCTGGCTGACTGAGGGTTTACCTCAGTTCGACACTACTG	224
1662	QY	GGAGTGTGTGTGGCGGAGAAAGACCCAGCTGGGTGATCGGGCTGGGCACAGAACCGCAAG	172
225	Db	GGAGTGTGAGGTGGCGGACAGACCCACTGGGCAGTGGGTGATGTCGGGACTCCGTGAG	284
1722	QY	CGCAAGGGCAGATCCAGATCCAGCCAGCGCGGCTTCTTACTGCACTCGTGATGCACGA	178
285	Db	CCGAAAGGGCGAGTTGACTCCACTCCCTGAGACTGGCGGGTGGCGGCTATGGAA	344
1782	QY	TGGCAACCAAGTACACGGCTGCACGGAGCGCTTGGACGGCGCTTAACGTCGGGCACAACT	184
345	Db	TGGGACAAATATGACGCCACACACACCTTTTACCCCTTTTGACATCAAGGTGAAC	404
1842	QY	TGACAAGGTGGGTGTCCTCTGGACTATGACCAAGGCTTGCTCATCTTCTACAATGCTGA	190
405	Db	CAAAGCGGTAGGCATATTTCTTAGACTATGAGCGCGGCACACTGTCTTTCTACAATGTCA	464
1902	QY	TCACATGTCCTGGCTCTACACCTTCCGGAGAAAGTTCCCTGGCAAGCTCTGCTCTTACTTT	196
465	Db	AGACCGCTCTCATATCTACACCTTCACTGATACTTTTACTGAGAAACTTTGGCCCTCTTT	524
1962	QY	CAGCCCTGGC	1971
525	Db	CTAGCCAGGC	534

RESULT 13

US-10-120-988-277 ; Sequence 277, Application US/10120988
: Publication No. US20030219745A1

; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyun
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 277
; LENGTH: 3038
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1557)
US-10-120-988-277

Query Match
Best Local Similarity 3.5%; Score 132.4; DB 16; Length 3038;
Matches 265; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

QY	1486	GCGCCCTAACCTGGACCGGGGACAGCCACAGCGCCGTGATCTCGGACGACTGC	1545
Db	1009	GGGAGTGACCTGGACCGGGGACAGCCACAGCGCCGTGATCTCGGACGACTGC	1068
QY	1546	ACCAATTGGCTTACGGCACTTGCACCCACAGCCACAGCGCCGTGATCTCGGACGACTGC	1605
Db	1069	AGAGCGTCAAGTTGCGGAGACAAGACTCGGGATCTCCCTGACACACAAAGCGTTTC	1128
QY	1606	GATGTGGAGGTGCGGTGCTTGAAGCCCTTCAAGCTTCAAGTGTGCGTCCACTACTGGGAG	1665
Db	1129	ACCTTCTACCTTTGGCTGCTGGCTACTGAGGTTTCACTCAGTGACACTACTGGGAG	1188
QY	1666	GTGCTGGTGGGAGAGACCCAGTGGGTGATCGGGTGGCAACAGCGCCGCAAGCCGC	1725
Db	1189	GTGAGTGGGGGACAGACCCAGTGGGTGATCGGGTGGCAACAGCGCCGCAAGCCGC	1248
QY	1726	AAGGGCAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGATCTGTGACGATGGC	1785
Db	1249	AAGGGCAGTTGACTCCACTCCCTGAGACTGGCTACTGGCGGTGCGGCTATGGAATGG	1308
QY	1786	AACCAATAGCGCTTGCAGCGGACCCCTGGACCGGCTTAACTCCGGGACAAAGTTGAC	1845
Db	1309	GACAAATATGACGCCACCAACACCTTTTACCCCTTTGACATCAAGTGAACCAAG	1368
QY	1846	AAGTGGGTGCTTCTGACATGACCAAGGTTGCTCATCTTCAATGATGATGAC	1905
Db	1369	CGGTAGGCATATCTAGCATATGAGCGGGGACACTGTCTTTTACAAATGTCACAGAC	1428
QY	1906	ATGTCTGTGCTTACACCTTCCGCGAGAAGTTCCCTGGCAAGCTCTGCTTACTTACG	1965
Db	1429	CGCTCTCATATCTACCTTCACTGATCTTTTACTGAGAACTTTGGCCCTCTTCTAC	1488
QY	1966	CTGGC 1971	
Db	1489	CCAGGC 1494	

RESULT 14

US-10-104-047-103
; Sequence 103, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA

; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 1904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-103

Query Match
Best Local Similarity 3.2%; Score 122.8; DB 16; Length 1904;
Matches 519; Conservative 0; Mismatches 602; Indels 15; Gaps 2;

QY	893	ACAAGGTCAAGCTCTTCTGCTCAGGACCGCGGCTTCTCTGCTTCTTCTGCGACGAGC	952
Db	1	ACCGCTGAGCATCTACTGCGAGCAGACCGCGGCTGCTGCGGAGTGTGCGCTCAC	60
QY	953	CTGCATCTGCAGCAGCATCAGGTCAACCGCATCGAGCGCTTCAAGACAGCGAGTGCAGA	1012
Db	61	TCGCTCGCACCGCGGTCTGCTCTGCTGCGCGGAGGCCACGACGCTCAAGA	120
QY	1013	GGGAGCTGAAGGACCAACTTCAAGCCCTTCAAGACAGCGAGCGGGAACACACCGAAGCG	1072
Db	121	CACAGCTGCCACAGCAGAAATGTCAGCTGAGGAGGATGTCATCGTAAAGGAGAGTG	180
QY	1073	TGCAGCTGCTCAAGCAGCAACTGCGGAGACCAAGTCTTCAACAGAGCCTTGGGACCA	1132
Db	181	TGGCTGTCTGGAGCATCAGCTGGTGGAGTGAGGAGAGAGTGCCTGAGTCCGGGGG	240
QY	1133	CTATCGCGGAGGCTTCGAGCGGCTGCACCGGCTGCTGCTGAGACCGCAGAGCCATGC	1192
Db	241	CCGTGGGGAGCAGCTGGGCAAGATCGGGTGTTCCTGGCTGCACTGGAGGGTCTCTTG	300
QY	1193	TAGAGGAGTGGAGGGGACACCGCGCGCACCGCTGACCGACATCGAGCAAGAGTCCAGC	1252
Db	301	ACCGCAGGAGCAGCGTGTACCGGGTGAGGACGAGGCTTGGCGCGGAGCTGGGGA	360
QY	1253	GCTACAGCAGCAGCTGCGCAGGCTCCAGGAGGAGCCAGATCTCTGAGAGGGGTGG	1312
Db	361	GCTGAACTTACCTGGAGCAGCTCGGAGATGGAGAAGTCTCTGGAGAGGTGGCGG	420
QY	1313	CTGAACCGACCGGACACCTTCTGCTGGGTGGCTCACTGTCCGAGCGCTCAAGG	1372
Db	421	ACAAGCGCAGACTGAGTTCTCATGAATACTGCTGCTGACCGACAGGCTGCAGAGA	480
QY	1373	GAAATATCATGAGACCAACCTCAATATGAAGACTTCCGACCTCCAAAGTACACAGGCC	1432
Db	481	TCCTGSCAGAGTCTCCCGCCACCGCCGCTGACATCCAGCTGCCAATATCTCAGATG	540
QY	1433	CCCTGAGTACCACTCTGGAAGTCCCTGCTCCAGACATCCACCGAGTCCAGCGCCC	1492
Db	541	ACTTCAATTCAGGTGTGGAGAGATGTTCCGGGCTCTGATGCGAGCGCTGGAGGAGC	600
QY	1493	TAACTTGGACCGGACAGCCACCGAGCTGATCTGCTGGAGCAGTGCACCATTTG	1552
Db	601	TGACCTTTGACCGAGCTCTGCGACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
QY	1553	TGGCTTACGGCACTTGCACCGACCGACCTGAGGACTCGGCAAGAGCGCTTCTGATG	1612
Db	661	TGGAGTGTCTGGGGGAGAGGCGCGCGGAGGACCGCGGAGGCTTTCGACAGG	720
QY	1613	AGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1672
Db	721	CGGTGGCGGTGCTGGGACCGACAGAGCTCTCCAGGGGCGAGCACTACTGGAGGTGG	780
QY	1673	TGGCGGAGAGAGCCAGTGGGTGATCGGGCTGGGACACAGAGCGCCGAGCGGAGGCA	1732
Db	781	TTGGCGACAGCGCGCTGGGCGCTGGGCGGTGATCGCGCGCGAGCGCGCGCGCGGCG	840

Mon Aug 2 10:03:37 2004

Qy	1733	GCATCCAGATCCAGCCACGCGGGCTTCTACTGCATCGTGATGCAAGTGGCA-----	1786
Db	841	GCCTGCACGGGTGCCCTCGCAGGGCTGTGGGTGTGGCGCGAGGGGCAAGATCC	900
Qy	1787	---ACCAAGTACAGGCGCTGTCACGAGCCCTGAGCGGGCTTAAAGTCCGGGCAAGCTTG	1843
Db	901	TGGAGGCACACGTGGAGGCCAAGAGCCGCGCGCTCTGCGCAGCCCGAGAGCGGCCCA	960
Qy	1844	ACAAGTGGGGTGTCTTCTCGAGCTATGACCAAGGCTTGCTCATCTTCTCAATGCTGATG	1903
Db	961	CGGCAATTGGCCTTTACTCTAGCTTCGCGACAGCGCTCTCTCCTCTTACGATGCCACGG	1020
Qy	1904	ACATGTCCTGGCTCTACACTT-----CCGCGAGAAGTTCCCTGGCAAGCTCTGCTCTT	1957
Db	1021	ACGCCGACGGCTCGTGGCGCTTTTGGCTTCCAGAGCGCTGCCAGGCCGTGTACC	1080
Qy	1958	ACTTCAGCCCTGGCCAGAGCCACCCAAATGSCAAGAAGCTTACGCCGTGGGATC	2013
Db	1081	CTTCTTCTCGAGCTGTGTGGCACACAAGGSCAAGAATGCCACGCCGTCTGTCT	1136

Search completed: July 31, 2004, 23:28:10
Job time : 1590 secs

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RESULT 15
US-09-731-872-225
; Sequence 225, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US3.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 225
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 171..1670
US-09-731-872-225

```

Query Match	3.2%;	Score 122;	DB 9;	Length 1739;
Best Local Similarity	51.9%;	Pred. No. 6.1e-23;		
Matches 300;	Conservative	0;	Mismatches 275;	Indels 3; Gaps 1;
1419	CAAGTACACAGGCCCCCTGCAGTACACCACTCTGGAAGTCCCTGTTCACGAGACATCCACCC	1478		
1070	CCAGTACAAAGTCTCTATCCAGTACATGTTATGGAGGGAATATCAGGACACTCTCTGCC	1129		
1479	AGTGCACAGCGCCCTAAACCTTGACCCCGGCGCACAGCCACCAGCGCCTGATCCTGTGCGA	1538		
1130	AGCCTGTCTCCACTAACTCTGACACCCCTAAACAGCTCACCCAAATCTGGTCTCTCCAA	1189		
1539	CGAGTGCACATTGTGGCTTAACGCCAACTTGCACCCACAGCCACTGACGAGACTCGCCAA	1598		
1190	AAGCCAAACCGCGTCTGGCATGGTGACATTAAGA---AGATAATGCTGATGATCCTGA	1246		
1599	GGCTTCGATGTGGAGGTGTCGTGCTGGGTTCTGAAGCCTTCAGTAGTGGCGTCCACTA	1658		
1247	GAGGTTTGACTCAAGTGTGGCTGTACTGGGCTCAAGAGGGTTTCAACCTCTGGAAAGTGTTA	1306		
1659	CTGGGAGGTGGTGGTGGCGGAGAAGACCCAGTGGGTGATCGGGCTGGCACACAGAAAGCCGC	1718		
1307	CTGGGAAGTAGAAGTAGCAAAAGAAACAATAATGACAGTTGGAGTTGTACAGAAATCCAT	1366		
1719	AAGCCGCAAGGGGAGCATCCAGATCCAGCCACCGCGGGTCTTCTACTGCGATGGTGATGCA	1778		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2004, 12:05:13 ; Search time 247 Seconds
(without alignments)
8596.122 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 agctgcgtgacgaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	2.8	3416	2	US-08-724-394A-15
2	95.8	2.5	1782	4	US-09-220-132-158
3	94	2.5	7218	1	US-08-232-463-14
4	86.4	2.3	2926	2	US-08-724-394A-13
5	86.4	2.3	2970	4	US-09-566-921-105
6	82.8	2.2	3502	2	US-08-724-394A-16
7	81.6	2.1	53526	3	US-08-658-136-2
8	81.6	2.1	53577	3	US-08-658-136-1
9	80.4	2.1	152331	3	US-09-128-155-16
10	76.2	2.0	1926	2	US-09-249-585A-4
11	76.2	2.0	1931	2	US-09-130-114-2
12	75	2.0	4897	6	5196516-7
13	74.6	1.9	3470	4	US-09-486-147-2
14	74.4	1.9	320	3	US-09-165-264-7
15	74.2	1.9	16891	4	US-09-486-147-1
16	74	1.9	543	4	US-09-486-147-4
17	73	1.9	320	3	US-09-165-264-13
18	73	1.9	2882	2	US-08-724-394A-12
19	72.8	1.9	320	3	US-09-165-264-11
20	72.8	1.9	12001	1	US-08-458-568A-11
21	71.8	1.9	320	3	US-09-165-264-14
22	70.2	1.8	319	3	US-09-165-264-8
23	70	1.8	318	3	US-09-165-264-12
24	69.6	1.8	712	4	US-09-401-064-354
25	63.6	1.7	77536	4	US-09-410-551B-1
26	62.6	1.6	2561	4	US-09-616-289-48
27	60.4	1.6	44377	2	US-08-804-227C-7

28	60.4	1.6	44377	2	US-08-804-198-1	Sequence 1, Appli
29	60	1.6	3227	4	US-09-620-312D-103	Sequence 103, App
30	59.4	1.6	697	3	US-09-040-984-17	Sequence 17, Appl
31	59.4	1.6	697	4	US-09-123-912-17	Sequence 17, Appl
32	59.4	1.6	697	4	US-09-643-597-17	Sequence 17, Appl
33	59.4	1.6	697	4	US-09-480-884A-17	Sequence 17, Appl
34	59.4	1.6	697	4	US-09-542-615A-17	Sequence 17, Appl
35	59.4	1.6	697	4	US-09-606-421B-17	Sequence 17, Appl
36	59.4	1.6	697	4	US-09-221-107-17	Sequence 17, Appl
37	58.6	1.5	1926	4	US-09-249-585A-2	Sequence 2, Appli
38	58.6	1.5	1926	4	US-09-410-399-3	Sequence 3, Appli
39	58.6	1.5	2580	3	US-09-050-863-2	Sequence 2, Appli
40	58.6	1.5	2580	4	US-09-359-081-2	Sequence 2, Appli
41	58.6	1.5	5452	2	US-09-130-114-1	Sequence 1, Appli
42	58.6	1.5	8705	4	US-09-647-344A-14	Sequence 14, Appl
43	58.6	1.5	9600	3	US-08-910-647-1	Sequence 1, Appli
44	58.6	1.5	9600	4	US-09-620-925-1	Sequence 1, Appli
45	58.6	1.5	10596	1	US-07-884-811-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-08-724-394A-15
; Sequence 15, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Rudy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereeto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..3416
; OTHER INFORMATION: /note= "cDNA 44"
US-08-724-394A-15

Query Match 2.8%; Score 106; DB 2; Length 3416;
 Best Local Similarity 53.8%; Pred. No. 7e-14;
 Matches 242; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy 1482 GCCAGCGCCCTAACCTGGAGCCGGGACAGCCACCAGCGCTGATCCTGTCGGACGA 1541
 Db |||||
 Qy 1373 GCCTGGGATGTGATCTGGATCCAAACAGCAACCCCACTCTCTCTGTTCTGAGGA 1432
 Db |||||
 Qy 1542 CTGCACCAATTGTGGCTTACGGCAACTTGCACCCACAGCACTGCAGGACTCGCCCAAGCG 1601
 Db |||||
 Qy 1433 CCAGAGGAGTGTGAGCGTGCCTAA--GGAGCCCCAGGATCTGCCAGCAACCTTGAGAG 1499
 Db |||||
 Qy 1602 CTTCGATGTGAGGTGTGGTGTCTGGTTCAGAGCCCTCAGTAGTGGCTCCACTACTG 1661
 Db |||||
 Qy 1490 ATTTAAATGGCAATTAATTGTCTCGGCTGTGAGAGCTTCATATCAGGGAGACATTACTG 1549
 Db |||||
 Qy 1662 GGAGTGTGTGTGGGAGAGACCCAGTGGTGTGATCGGGCTGGCACAGGAGCGCAAG 1721
 Db |||||
 Qy 1550 GGAGTGTGTGTGGGAGAGACCCAGTGGTGTGATCGGGCTGGCACAGGAGCGCAAG 1609
 Db |||||
 Qy 1722 CCAGAGGAGATCCAGATCCAGCCAGCGCGGCTTCTACTGATCGTGTGATGACGA 1781
 Db |||||
 Qy 1610 GAGAAAGGCTGGGTCAAAATGACACCTGAGATGATCTGGACTATGGGCTGACTGA 1669
 Db |||||
 Qy 1782 TGGCAACAGATACAGCGCTGACGAGCCCTGGACGGGCTTAACGTCCGGGACAGCT 1841
 Db |||||
 Qy 1670 TGGGAATAAGTATCGGACTCTAACTGAGCCAGCAACCACTGAACTCTTAAAGCCCC 1729
 Db |||||
 Qy 1842 TGCAAGTGGTGTCTTCTGGACTATGACCAAGGCTTGTCTCACTTCTACAATGCTGA 1901
 Db |||||
 Qy 1730 TAAGAAATGGGGTCTTCTGGACTATGAGACTGGAGATATCTCATCTACATGCTGT 1789
 Db |||||
 Qy 1902 TGACATGTCCTGGCTTACACTTCCGCGA 1931
 Db |||||
 Qy 1790 GGATGGATCGCATATTCATCTTCTCTGGA 1819
 Db |||||

RESULT 2
 US-09-220-132-158
 ; Sequence 158, Application US/09220132
 ; Patent No. 6506607
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
 ; FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 07334-074001
 ; CURRENT APPLICATION NUMBER: US/09/220,132
 ; CURRENT FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 60/079,303
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: US 60/069,821
 ; PRIOR FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 158
 ; LENGTH: 1782
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-220-132-158

Query Match 2.5%; Score 95.8; DB 4; Length 1782;
 Best Local Similarity 52.6%; Pred. No. 9.8e-12;
 Matches 233; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

Qy 1484 CAGCGCCCTAACCTGGAGCCGGGACAGCCACCAGCGCTGATCCTGTCGGAGACT 1543
 Db |||||
 Qy 1178 CAGTGGAGTGTGACTCTGGACCCAGACAGCGGCTACCCAGCGTGTCTCTGTGATAATC 1237
 Db |||||
 Qy 1544 GCACCAATGTGGCTTACGGCACTTGCACCCACAGCACTGAGGACTGCGCAAGCGCT 1603
 Db |||||
 Qy 1238 TGGCGGAAGTGGGTACAGTTAC---CTCAACAGGAGCTGCTGACCAACCCCGAGAGT 1294
 Db |||||

Qy 1604 TCGATGTGGAGTGTCTGGTCTTGAAGCCTTCAGTAGTGGGCTCCACTACTGGG 1663
 Db |||||
 Qy 1295 TCAATCTGTTTCCCTGTGTCTTGGGCTCTCCATGCTTCATGCGGGAGACATTTATGGG 1354
 Db |||||
 Qy 1664 AGTGTGTGTGGCGGAGAGCCAGTGGGTGATCGGGCTGGCACAGGAGCCGCAAGCC 1723
 Db |||||
 Qy 1355 AGGTAGAGGTGGGAGATTAAGCCAAAGTGGACCATAGGTGTCTGTGAAGACTTCAGTGTGCA 1414
 Db |||||
 Qy 1724 GCAAGGCGAGCATCCAGATCCAGCCAGCCGCGGCTTCTACTGCTGATCGTGTGACGATG 1783
 Db |||||
 Qy 1415 GAAAGGTGGAGTAACCTCAGCCCCCAGAAATGATTTCTGGGCAAGTGTCTTTTGTGGTATG 1474
 Db |||||
 Qy 1784 GCAACCAAGTACAGCGCTGACGAGCCCTGGACGCGGCTTAAAGTCCGGGACCAAGCTTG 1843
 Db |||||
 Qy 1475 GGAAGAAATATTGGGCTTCTTACCTCCCAATGATGCTCCCTACCCCTGGGACCCGCTCC 1534
 Db |||||
 Qy 1844 ACAAGTGGGTGTCTTCTCGGACTATGACCAAGGCTTGTCTCATCTTCTACAATGCTGATG 1903
 Db |||||
 Qy 1535 AGCGGTGGGAGATTTCTTGGACTATGATGCTGGTGGAGTCTCCTTCTTACCAACGTCAG 1594
 Db |||||
 Qy 1904 ACATGTCTGCTTACACCTTC 1926
 Db |||||
 Qy 1595 AGAGTGTACACCTTCACTTTC 1617
 Db |||||

RESULT 3
 US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232,463
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/935,313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZgpt-Fls
 US-08-232-463-14

US-09-566-921-105

Query Match 2.3%; Score 86.4; DB 4; Length 2970;
Best Local Similarity 52.7%; Pred. No. 1.3e-09;
Matches 236; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
QY 1483 CCAGCGCCCTTAAACCTGGACCGGGCACAGCCACAGCGCTGATCCTGCGAGAC 1542
Db 1220 CTTGGGATGATCTGGATCCAGACAGGCAACGCCATCCTCTGTTCTTGAGAC 1279
QY 1543 TGACCACTTGTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTGCCAAAGCGC 1602
Db 1280 CAGAGGAGTGTG---CAGCGTCTGAAGAGCGCGGGATCTGCCAGACAACCTTGAGAGA 1336
QY 1603 TTTGATGTGAGGTGTGGTCTGGTCTGAGGCTTGAAGCCTTCAGTAGTGGGTCCACTCTGG 1662
Db 1337 TTTGATGTGGGCTTACTGTCTGCTTGGCTGTGAAACTTTCATCAGGAGACATTAATCTGG 1396
QY 1663 GAGTGTGTGGTGGGGAGAGACAGCCAGTGGGTGATCGGCTGGCAC---ACGAGCCGCA 1719
Db 1397 GAGTGAAGTGGGGGACAGAAAGATGGCATATTGGGATATAGTAAGAACTGGAG 1456
QY 1720 AGCGCAAGGCGACATCCAGATCCAGCCACAGCCACTGCAGGCTTCTACTCATCGTATGCAC 1779
Db 1457 AGGAAAAAGGTGGCTCAAAATGACACCGGAGAACGATATGGAATCTGGGCTGACT 1516
QY 1780 GATGGCAACAGTACAGGCTGACCGAGCCCTGGAGCGGCTTAAGTCCGGGACAAG 1839
Db 1517 GATGGGAATAGTATCGGGCTCTCACTGAGCCCAAGAACCACTTCCCTGAGCCT 1576
QY 1840 CTTGACAAAGTGGGTGTCTTCTGGACTATGACCAAGCTTGTCTCATCTTCTACAAATGCT 1899
Db 1577 CCTAGGAAGTGGGGATCTTCTGGACTATGAGACTGGAGAGATCTGTTCTTAATAGCC 1636
QY 1900 GATGACATGTCTGGCTTACACCTTCC 1927
Db 1637 ACAGATGATCTCATATCTACACCTTTC 1664

RESULT 6

US-08-724-394A-16
Sequence 16, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kromal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchibashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3502 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..3502
OTHER INFORMATION: /note= "cDNA 32"
US-08-724-394A-16

Query Match 2.2%; Score 82.8; DB 2; Length 3502;

Best Local Similarity 52.2%; Pred. No. 8.8e-09;
Matches 233; Conservative 0; Mismatches 207; Indels 6; Gaps 2;

QY 1484 CAGCGCCCTTAAACCTGGACCGGGCACAGCCACAGCGCTGATCCTGCGAGAC 1543
Db 1063 CTGCTGATGTGGTCTCGATCCAGACACCGCTCATCCGAGCTCTTCTGTGAGAGACC 1122
QY 1544 GCACCATTTGGCTTACGGCAACTTGCACCCACAGCCACTGCAGGACTCGCCAAAGCGCT 1603
Db 1123 GGAGAGTGTGAGCGGGGGCCCT---ACAGGCAGAGAGTGCCTGACAACCCAGAGAT 1179
QY 1604 TCAGTGTGAGGCTGCTCGGTGCTGGGTTCTGAAGCCTTCAGTAGTGGGTCCACTACTGGG 1663
Db 1180 TGACACTCAGCCTTGTGCTCTGGATGGGAGAGCTTCGCTCAGGGAACATTAATCTGGG 1239
QY 1664 AGTGTGTGGTGGGAGAAAGACCCAGTGGGTGATCGGGCTGGGACACAGAACCCGCAAGCC 1723
Db 1240 AGTGTGAGGTGGAAACGCTGATGTGTGACTGTGGGGGTCTGCAGACACAGTGTGAGA 1299
QY 1724 GCAGGCGCAGCATCCAGATCCAGCCACAGCGCGCTTCTACTGATCGTGTGACCATG 1783
Db 1300 GGAAGGGGAGGTCTCTGCTGATTCCTCAGAAATGGCTTCTGGACCTGGAGATG---TTTG 1356
QY 1784 GCACCAAGTACAGCGCTGCACGAGCGCTGGAGCGCGCTTAAAGTCCGGGACAAGCTTG 1843
Db 1357 GAACCAATACCGGGCCCTGTCTCCCTGAGAGGATTCCTCCCTTGAAGGAGTCCCTTT 1416
QY 1844 ACAAGTGGGTGTCTTCTCGACTATGACCAAGCTTGTCTCATCTTCTACATGCTGATG 1903
Db 1417 GCGGGTGGGCGTCTTCTCGACTATGAACTGGAGATGTCTCTTCTACAAATGAGGG 1476
QY 1904 ACATGCTCTGCTCTACACCTTCGC 1929
Db 1477 ACAGTACACATCTACATGTCCC 1502

RESULT 7

US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS

Db 887 CTCGTCCTCCCGTCTCTCCCGTCTCTCGTCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCTC 946
QY 835 TTCCCGTGGAGGCACTCTCAACG 894
Db 947 CCGGTCT 1006
QY 895 AAGTCAAGCT 954
Db 1007 CGGCCCCAGCT 1066
QY 955 GCATGCGAC 963
Db 1067 CTCCTGCGAC 1075

RESULT 12
5196516-7
; Patent No. 5196516
; APPLICANT: SCHREURS, CHRISTA S.; METTENLEITER, THOMAS C.
; SIMON, ARTUR J.; LUKAS, NOEMI; RZIHA, HANNS J.
; TITLE OF INVENTION: PSEUDORABIES VIRUS VACCINE
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/383,833
; FILING DATE: 21-JUL-1989
; SEQ ID NO: 7;
; LENGTH: 4897
; 5196516-7

Query Match 2.0%; Score 75; DB 6; Length 4897;
Best Local Similarity 48.1%; Pred. No. 5.1e-07;
Matches 243; Conservative 0; Mismatches 260; Indels 2; Gaps 1;
QY 103 CCCCT 162
Db 3767 CCGTCTCCCGTCT 3826
QY 163 CAGGATTCCT 222
Db 3827 CCGTCT 3886
QY 223 CCGCT 282
Db 3887 CCGTCT 3946
QY 283 CTGCG 342
Db 3947 CCGTCT 4006
QY 343 C--TCCAGCG 400
Db 4007 CCGTCT 4066
QY 401 CCGTCT 460
Db 4067 CCGTCT 4126
QY 461 CCGTCT 520
Db 4127 CCGGCGTCT 4186
QY 521 CCGTCT 580
Db 4187 CCGTCT 4246
QY 581 CCGTCT 605
Db 4247 CCGTCT 4271

RESULT 13
US-09-486-147-2
; Sequence 2, Application US/09486147

QY 955 GCATGCGAC 963
Db 1067 CTCCTGCGAC 1075
RESULT 11
US-09-130-114-2
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/ID903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

Query Match 2.0%; Score 76.2; DB 2; Length 1931;
Best Local Similarity 44.4%; Pred. No. 2e-07;
Matches 350; Conservative 0; Mismatches 438; Indels 1; Gaps 1;
QY 176 CCGCAGCT 235
Db 287 CTCCT 346
QY 236 TCCACCGCT 295
Db 347 CTCCT 406
QY 296 TAGAACCT 354
Db 407 GTCT 466
QY 355 ATCGCT 414
Db 467 CCGCT 526
QY 415 TCAGCG 474
Db 527 CTCGTCT 586
QY 475 GSTAGCT 534
Db 587 GTCT 646
QY 535 CCGACAGCG 594
Db 647 CTCCT 706
QY 595 CCGTCT 654
Db 707 CTCGTCT 766
QY 655 TACAGAGCGCGGTGAGCT 714
Db 767 CTCCT 826
QY 715 CATCT 774
Db 827 CTCCT 886
QY 775 GCGAGCGCGCGGTGCG 834

Patent No. 6627745
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as
APPLICANT: represented by the Secretary, Department of Health and Human
APPLICANT: Services
APPLICANT: Daniel L. Kastner
APPLICANT: Ivona Aksentijevich
APPLICANT: Michael Centola
APPLICANT: Zuoming Deng
APPLICANT: Raman Sood
APPLICANT: Francis S. Collins
APPLICANT: Trevor Blake
APPLICANT: P. Paul Liu
APPLICANT: Deborah Gumucio
APPLICANT: Robert I. Richards
APPLICANT: Darrell O. Rieke
APPLICANT: No. 6627745man A. Doggett
APPLICANT: Moraechai Pras
TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
FAMILIAL MEDITERRANEAN FEVER
FILE REFERENCE: 14014.0314U1
CURRENT APPLICATION NUMBER: US/09/486,147
CURRENT FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: PCT/US98/17255
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: 60/056,217
PRIOR FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3470
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
US-09-486-147-2

Query Match 1.9%; Score 74.6; DB 4; Length 3470;
Best Local Similarity 50.1%; Pred. No. 5.5e-07;
Matches 241; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
QY 1493 TAACCTTGGACCGGGGACAGCCACAGGAGCTGCGCAAGCGGCTTCGATGCG 1552
Db 1799 TGATCTGGATGTCAGAAACCGCTTACCCCAACCTCATCTCTCTGATGATCTGAAGAGTG 1858
QY 1553 TGGCTTACGGCACTTGCACCCACAGCACTGCAGGAGCTGCGCAAGCGGCTTCGATGCG 1612
Db 1859 TTAGACTTGAAC---AAGTGGAGAGGCTGCTGATGCGCCGCAAGATTTGACAGCT 1915
QY 1613 AGGTGTCGTGCTGGGTCTTGAAGCCTTCAAGTGTGCGCTCCACTACTGGGAGGTGGTG 1672
Db 1916 GTATCATTTGTTCTGGGCTCTCCGAGTTTCTCTCTGCGCGCGTTACTGGGAGGTGGAGG 1975
QY 1673 TGGGGNAGAGACCCAGTGGGTATCGGGTGGGACAGAGCGGCAAGCGGCAAGCGGCA 1732
Db 1976 TTGGAGACAAGACAGCATGATGCTTGGAGCGCTTCAAGACATCCATAAGCAGGAAAGGGA 2035
QY 1733 GCATCCAGATCCAGCCCGCGGCTTCTACTGATGATGATGATGATGATGATGATGATGAT 1792
Db 2036 ACATGACTCTGTCCGACAGAAATGGCTACTGGGTGGTGAATGATGATGATGATGATGATGAT 2095
QY 1793 ACAGCGCTCGACGAGCGCTGACGCGGCTTAACGTCGCGGACAAAGCTTTGACAAGGTGG 1852
Db 2096 ACCAGGCGTCAGCGTTTCCCGGACCGCGCTGTCTAATAAGAGAGCGCTCCCAAGCGTGG 2155
QY 1853 GTGCTTCTGGACTATGACCAAGGCTTGCTATCTTCTACATGCTGATGATGATGATGATGAT 1912
Db 2156 GCATCTTCTGGACTACAGATTTGAGATCTCTTTTACATGATGATGATGATGATGATGATGAT 2215
QY 1913 GGCTTACACCTT---CCGCGAGAAGTTCCCTGGCAGCTCTGCTCTTACTTTCAGCCCTG 1969
Db 2216 ACATCTATACATTCGCGAGCTGCTTCTTCTGCGGCGCTTCAACCTATCTTTCAGCCCTG 2275
QY 1970 G 1970

Db 2276 G 2276

RESULT 14

US-09-165-264-7/c
Sequence 7, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-7

Query Match 1.9%; Score 74.4; DB 3; Length 320;

Best Local Similarity 52.2%; Pred. No. 2.7e-07;
Matches 165; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 136 ACGGCTCGGCTGCTGCTCCCTCCCTCCAGGATTTCCCATCCCGAGCTTCTTCGCGCTCC 195
Db 316 AGGCGATGGCTAGCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 257
QY 196 GCGACCGCGCCACCCCGGAGTTTCGACCCCTTAAAGGCTTCACCCCGCTCCGGGATCC 255
Db 256 CCG 197
QY 256 CTTTCTCCAGCTCTATCTTCTAGGACTGCGCGCGCGCGCTAGAACCTCCCGCTCAGGAT 315
Db 196 CCG 137
QY 316 CTGCTGCTCTCAGCGCTCAGCGCTCTCTCCACGCGCCATCGCTTTGAGTGGCCACTA 375
Db 136 CCG 77
QY 376 CTTCTAGACTGCTCTCCGCGCTGCGGCTCCGACGAGTCTCAGCGCGGACCCCTTCTCTC 435
Db 76 CCG 17
QY 436 GCGTTACCTCTCTTCC 451
Db 16 CCG 1

RESULT 15

US-09-486-147-1
Sequence 1, Application US/09486147
Patent No. 6627745
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as
APPLICANT: represented by the Secretary, Department of Health and Human
APPLICANT: Services
APPLICANT: Daniel L. Kastner
APPLICANT: Ivona Aksentijevich
APPLICANT: Michael Centola
APPLICANT: Zuoming Deng
APPLICANT: Raman Sood
APPLICANT: Francis S. Collins
APPLICANT: Trevor Blake
APPLICANT: P. Paul Liu
APPLICANT: Deborah Gumucio
APPLICANT: Robert I. Richards
APPLICANT: Darrell O. Rieke
APPLICANT: No. 6627745man A. Doggett

```
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16891
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: n = a, t, c, or g
US-09-486-147-1

Query Match      1.9%; Score 74.2; DB 4; Length 16891;
Best Local Similarity 49.9%; Pred. No. 1.1e-06;
Matches 240; Conservative 1; Mismatches 234; Indels 6; Gaps 2;

QY 1493 TAACTCTGACCCGGGACACAGCCACCGCGCTGATCTGTGGACGACTGCAACCATTTG 1552
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QY 13903 TGATTCTGATCAGAAACCGCTTACCCCAACCTCTCTCTGATGATCTGAAGAGTG 13962
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QY 1553 TGGCTTACGGCACTTGACCCACAGCCACTGCGCAAGCGCTTCGATGTGG 1612
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QY 13963 TTAGACTTGGAAAC---AAGTGGGAGAGGCTGCCTGATGCCCGCAAGATTGACAGCT 14019
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QY 1613 AGGTGTCGCTGGCTTCTGAAGCCTTCAGTAGTGGCGCTCCACTACTGGGAGGTGGTGG 1672
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QY 1673 TGGCGGAGAGACCCAGTGGGTGATCGGCTGGGCACACGAAAGCCGCAAGCCGCAAGGCA 1732
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1733 GCATCCAGATCCAGCCAGCCGCGCTTCTACTGATCGTGATGCACGATGGCAACCACT 1792
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QY 14140 ACATGACTCTGTGCCAGAGAATGGCTACTGGGTGGTGATATGATGAAGGAAATGAGT 14199
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QY 1793 ACAGCGCTGCACGGAGCCCTGGACGCGGCTTAACGTCGGGACAAAGCTTTGACAGGTGG 1852
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QY 14200 ACCAGCGTCCAGCGTTCCCGGACCCGCGCTGCTAATAAGGAGCCTCCCAAGCGTGG 14259
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1853 GTGTCTTCTGGACTANGAACAGGCTTGCTATCTTCTACATGCTGATGATGATGCTCT 1912
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QY 14260 GCATCTTCTGGACTACAGAGTTGGAAGCATCTCTTTTACATGTGACAGCCRGATCCC 14319
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QY 1913 GGCCTTACACCTT---CCGCGAGAGTTCCTGCGCAAGCTCTCTTCTTCTCAGCCCTG 1969
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QY 14320 ACATCTATACATTGGCAGCTGCTCTTTCTCTGGGCCCTTCAACCTATCTTCAGCCCTG 14379
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QY 1970 G 1970
Db 14380 G 14380
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Job time : 250 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: ~ July 23, 2004, 15:08:11 ; Search time 46 Seconds
(without alignments)
3233.658 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
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Scoring table: BLOSUM62
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Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1312	52.4	304	9	US-09-927-091-2
3	613	24.5	500	9	US-09-731-872-466
4	613	24.5	500	10	US-09-876-997-466
5	583	23.3	580	9	US-09-925-301-943
6	550.5	22.0	485	14	US-10-276-372-2
7	550.5	22.0	485	16	US-10-473-576-1
8	541.5	21.6	485	15	US-10-094-749-2615
9	501	20.0	471	15	US-10-104-047-3482
10	500	20.0	468	15	US-10-104-047-3664
11	499.5	19.9	4675	15	US-10-093-463-74
12	492	19.6	465	14	US-10-024-298A-97
13	492	19.6	465	14	US-10-042-211A-97
14	492	19.6	465	16	US-10-617-217A-97
15	489	19.5	465	14	US-10-024-298A-99

16	489	19.5	465	14	US-10-042-211A-99	Sequence 99, Appl
17	489	19.5	465	16	US-10-617-217A-99	Sequence 99, Appl
18	475.5	19.0	4691	15	US-10-093-463-72	Sequence 72, Appl
19	427.5	17.1	395	15	US-10-108-260A-4617	Sequence 4617, Ap
20	418	16.7	475	12	US-10-042-865-65	Sequence 65, Appl
21	418	16.7	475	14	US-10-000-897-78	Sequence 78, Appl
22	418	16.7	475	15	US-10-094-749-2393	Sequence 2393, Ap
23	414.5	16.6	488	12	US-10-221-625-82	Sequence 82, Appl
24	411	16.4	483	12	US-10-114-270-106	Sequence 106, App
25	409	16.3	579	12	US-10-042-865-6	Sequence 6, Appli
26	408	16.3	592	12	US-10-042-865-64	Sequence 64, Appl
27	407.5	16.3	474	15	US-10-104-047-3289	Sequence 3289, Ap
28	393	15.7	498	14	US-10-247-671-167	Sequence 167, App
29	388.5	15.5	194	9	US-09-764-868-1031	Sequence 1031, Ap
30	388.5	14.7	277	15	US-10-094-749-3098	Sequence 3098, Ap
31	364.5	14.6	413	12	US-09-978-360A-710	Sequence 710, App
32	364.5	14.6	413	14	US-10-319-763-198	Sequence 198, App
33	343.5	13.7	183	9	US-09-864-761-36547	Sequence 36547, A
34	341	13.6	630	16	US-10-408-765A-640	Sequence 640, App
35	341	13.6	630	16	US-10-317-277A-168	Sequence 168, App
36	340.5	13.6	438	15	US-10-262-445-34	Sequence 34, Appl
37	339	13.5	584	9	US-09-910-174A-16	Sequence 16, Appl
38	339	13.5	584	9	US-09-955-866-12	Sequence 12, Appl
39	339	13.5	584	9	US-09-896-738-18	Sequence 18, Appl
40	339	13.5	584	14	US-10-041-319-17	Sequence 17, Appl
41	339	13.5	584	16	US-10-648-593-157	Sequence 157, App
42	339	13.5	584	16	US-10-644-671-16	Sequence 16, Appl
43	334.5	13.4	333	15	US-10-104-047-2073	Sequence 2073, Ap
44	329	13.1	513	9	US-09-910-174A-18	Sequence 18, Appl
45	329	13.1	513	16	US-10-644-671-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-927-091-1
; Sequence 1, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: USPC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
US-09-927-091-1

Query Match	100.0%;	Score	2504;	DB	9;	Length	475;
Best Local Similarity	100.0%;	Pred. No.	7.1e-202;				
Matches	475;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MACSLKDELLCSICLSIYQDPSVLGCEHYFCRCITEHWVRQEAQAGARDCECRRTFAEP	60				
Qy	61	ALAPSLKIANIVRYSSFPDLAILNARRAAPQAHDKVKLFCLTDEALLCFRCDEPALH	120				
Db	61	ALAPSLKIANIVRYSSFPDLAILNARRAAPQAHDKVKLFCLTDEALLCFRCDEPALH	120				
Qy	121	EQHVTGIDDAFDELQREKLDQLQALQDSREHTEALQLLKQLAETKSKTSKSLRTTIGE	180				

Db 121 EQHQTGDDAFDELQRLKDLQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGE 180
QY 181 APERHLRLRRQKAMLELEADTARTLTDIEQKVORYSQQLRKVQEGAQILQERLAETD 240
Db 181 APERHLRLRRQKAMLELEADTARTLTDIEQKVORYSQQLRKVQEGAQILQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
Db 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
QY 301 PGTAHORLILSDCTIVAYGNLHPQLQDSERHTEALQLLKRQLAETKSTKSLRTTIGE 360
Db 301 PGTAHORLILSDCTIVAYGNLHPQLQDSERHTEALQLLKRQLAETKSTKSLRTTIGE 360
QY 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVVFL 420
Db 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVVFL 420
QY 421 DYDQGLLIFYNADDSWLYTFRKPGKLCVSFSGSHANGKNVQPLRINTVRI 475
Db 421 DYDQGLLIFYNADDSWLYTFRKPGKLCVSFSGSHANGKNVQPLRINTVRI 475

RESULT 2

US-09-927-091-2
; Sequence 2, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: UTSC:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Human
US-09-927-091-2

Query Match 52.4%; Score 1312; DB 9; Length 304;
Best Local Similarity 91.8%; Pred. No. 7.2e-102;
Matches 257; Conservative 2; Mismatches 5; Indels 16; Gaps 1;
QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARP 60
Db 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARP 60
QY 61 ALAPSLKUNIVERYSSFFPDALLNARRAARPCQAHDKVKLCLTDRLALCFCDPEPALH 120
Db 61 ALAPSLKUNIVERYSSFFPDALLNARRAARPCQAHDKVKLCLTDRLALCFCDPEPALH 120
QY 121 EQHQTGDDAFDELQRLKDLQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGE 180
Db 121 EQHQTGDDAFDELQRLKDLQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGE 180
QY 181 APERHLRLRRQKAMLELEADTARTLTDIEQKVORYSQQLRKVQEGAQILQERLAETD 240
Db 181 APERHLRLRRQKAMLELEADTARTLTDIEQKVORYSQQLRKVQEGAQILQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300
Db 241 RHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 300

RESULT 3

US-09-731-872-466
; Sequence 466, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78-US3-REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pgm
; SEQ ID NO 466
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-731-872-466

Query Match 24.5%; Score 613; DB 9; Length 500;

Best Local Similarity 31.6%; Pred. No. 9.5e-43;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;
QY 8 ELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQARDCEPCRRTFARPALAPSLK 67
Db 38 ELHCPCLCNDFRDLMLSCGHNFCEACIQDFWRLOAKE--TFCPECKMLCOYNNCTFNPV 95
QY 68 LANIVERYSSFFPDALLNARRAARPCQAHDKVKLCLTDRLALCFCDPEPALH--EQHQ 124
Db 96 LDKVKEIKKKPL-----LKGHPQCEHGENIKLFSKPDGKGLICFCQKDAKLSVQSKKE 149
QY 125 VTGIDDAFDELQRLKDLQALQDSEREHTEALQLLKRQLAETKSTKSLRTTIGSAFER 184
Db 150 FLQISDAVHFFMEELAIQQGQLETTIKELQTLRNQKEAIAAHKENKHLHQHVSMEFLK 209
QY 185 LHRLLRERQKAMLELEADTARTLTDIEQKVORYSQQLRKVQEGAQILQERLAETDRHTF 244
Db 210 LHQFLHSKEKDILTRELREGKALNEEMELNSQLOEQCLLAKDMLVSIQAKTEQQNSFDF 269
QY 245 LAGVASLSERLKG--KIHET-NLTVEDPPTSKYTGPLYTTIWSLFDIHPVPAALTLD 301
Db 270 LKDIITLLHSLEQGMKVLATRELISRKUNLGQYKGIQYMWVREMQDTLCFGLSPLTLD 329
QY 302 GTAHORLILSDCTIVAYGNLHPQLQDSERHTEALQLLKRQLAETKSTKSLRTTIG 361
Db 330 KTAHFNVLKSKQTSVWHGDI-KKIMPDDPERFSDSSVAVLSRGFTSGKWKYWEVVAKKT 388
QY 362 QWVIGLAHEAASRKSGSIQIOPSRGFCYIVMHDGNQYSACTEPWTRLNVDRKDKGVVFL 421
Db 389 KWTGVVRESIIRKSCPLTPEQGFWLLRLNQDTLKDALDFSLSLTLNNDKVGIYLD 448
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Db 449 YEGGQLSFYNKATWTHIYTFSTFMKLYPYFCPCINDGR-ENKPELHI 496

RESULT 4

US-09-876-997-466
; Sequence 466, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78-US4-CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872

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; ; PRIORITY FILING DATE: 2000-12-07
; ; PRIORITY APPLICATION NUMBER: US 60/197,470
; ; PRIORITY FILING DATE: 2000-03-06
; ; PRIORITY APPLICATION NUMBER: US 60/169,629
; ; PRIORITY FILING DATE: 1999-12-08
; ; NUMBER OF SEQ ID NOS: 482
; ; SOFTWARE: Patent.pm
; ; SEQ ID NO 466
; ; LENGTH: 500
; ; TYPE: PR1
; ; ORGANISM: Homo sapiens
; ; ORGANISM: Homo sapiens
US-09-876-997-466

Query Match      24.5%; Score 613; DB 10; Length 500;
Best Local Similarity 31.8%; Pred. No. 9.5e-43;
Matches 148; Conservative 83; Mismatches 222; Indels 16; Gaps 8;

QY      8  ELLCSICLSIYQDPVSLGCEHYFCRCITEHWRVQEAQAGARDCEPCRTTFAEPALAPSLK 67
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QY      68  LANIVERSYSPFDALINARRAARPCOAH-DKVKLFCLTDRLALCFCDPEPALH--EQHQ 124
Db      96  LDKLVEKIKKLP-----LKGHPQCPHGENLKFSPDKGLICFOCKDARLSVGOSKE 149
QY      125  VTGIDDAFDELQELKDQALQDSREHTEALQILKROLAETKSTKSLRTTIGEAER 184
Db      150  FTQISDAVHFFBEELAIQOQGLTTELKQTLNMQKEAIAHKNKHLHQHVSMEFLK 209
QY      185  LHLRLREROKAMLEEAADTARTLTIDQKVQYSQOLRVQGAQILQBLAETDRHTF 244
Db      210  LHQFLHSKEKDIILREBEGKALNEEMNLSQLQECLLAKDMLYSIQAKTEQONSFFD 269
QY      245  LAGVASLSRLKG--KIHTET-NUTYEDFPSTKYTGLOPYTIWKSFLQDHPVPAALTLDP 301
Db      270  LKDIITLLHSLEQGMKVLATRELISRKLNGLQYKGPQYVWVREMODTLCPGLSLPLTLD 329
QY      302  GTAHQBLIISDDCTIVAYGNLHPQLODSPKRTDVEVSLGSEAFSGVHYWVVAEKT 361
Db      330  KTAHPLNLVLSKSTSVWHGDI--KKIMDDPDEREDSSVAVLGSRGFTSGKWYWEVEVAKT 388
QY      362  QWVIGLAHAASRKGSIQIOPSRGFCYIVMHDGNQYSACTEPTWRLNVRDKLVGVFELD 421
Db      389  KWTGVVRSIRIKGSCPLTPEGFWLLRLNRQNTDLKALDLPFSFLTNNLDKVGILYLD 448
QY      422  YPQGLLIFYNADMSWLYTFREKPKGLCSYFSGQSHANGKNVQPLRI 470
Db      449  YEGGQLSFYNAKTMTHTIYTFNTFMEKLYPFYFCPLNDGR-ENKEPLHI 496

RESULT 5
US-09-925-301-943
; Sequence 943, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 943
; LENGTH: 580
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (52)

; ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; ; NAME/KEY: SITE
; ; LOCATION: (73)
; ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-943

Query Match      23.3%; Score 583; DB 9; Length 580;
Best Local Similarity 29.1%; Pred. No. 3.9e-40;
Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

QY      5  LKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWRVQEAQAGARDCEPCRTTFAEPALAP 64
Db      77  LQOETTCVCLQYFAEPMMLDCGHNICCAACARCWGTAETNVS--CPQCRETTPQSHMRP 134
QY      65  SLKANIVERSYSPFDALINARRAARPCOAH-DKVKLFCLTDRLALCFCC 114
Db      135  NRHLANVTQ-----LVKQLRTERPSGPGGEMGVCEKREPLKLYCEDQMPICVVC 185
QY      115  DEPALHEQHOVTGIDDAFDELQELKDQALQDSREHTEALQILKRO-----LAE 166
Db      186  DRSREHGHSHVLPLEAVEGFEQIQNL-----DHLKRVKDLKRRRAQGEQARAE 237
QY      167  TKSSTKSLRTTIGEAERLHRLRE---RQKAMLEBLE-----ADTA 205
Db      238  LLSLTQMEREKIWFEEQYVHSLKEHEYRLARLEELDIAIYNSINGAITQFSCNISHLS 297
QY      206  RTUTDIEQKVQYSQOLRVQGAQILQBLAETDR-----HTFLAGV 248
Db      298  SLIAQLEERQOQPTREL-----LDIGDTLSAERIRIPEPWITPPDLQEKIHIQAQC 351
QY      249  ASLSERLKKIKHETNLTIEDFTSKYTGLOPYTIWKSFLQDHPV---PAALTLDPGTAH 305
Db      352  LFLUTESLK-----QFTEKQMSMEK--IQELREAQIYSVDVTLDEDTAY 393
QY      306  QRILISDDCTIVAYGNLHPQLODSPKRTDVEVSLGSEAFSGVHYWVVAEKTQWVI 365
Db      394  PSLISLNDLRQVRYSLQ-QDLPDNEPERNLPCVLGSPCFIAGRIHWEVEVGDAKWTI 452
QY      366  GLAHEAASRKGSIQIOPSRGFCYIVMHDGNQYSACTEPTWRLNVRDKLVGVFELYDQG 425
Db      453  GVCEDSVCRKGGVTSAPQNGFWAVSLWYKEYWALTSPMTALPLRTPLQRVGIFLDYDAG 512
QY      426  LLIFYNADMSWLYTF-REKPKGLCSYFSGQSHANGKNVQPLRI 470
Db      513  EVSFYNVTERCHTFTFSHATFCQVPRYPFS--LSYSGGKSAAPLII 556

RESULT 6
US-10-276-372-2
; Sequence 2, Application US/10276372
; Publication No. US20030186269A1
; GENERAL INFORMATION:
; APPLICANT: Bahr, Georges
; APPLICANT: Cocude, Cecile
; APPLICANT: Capron, Andre
; TITLE OF INVENTION: SSA-56 kDa Polypeptide and its Fragments and Polynucleotides
; FILE REFERENCE: 017753-171
; CURRENT APPLICATION NUMBER: US/10/276,372
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: FR 00/06315
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/FR 01/00725
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-276-372-2

Query Match      22.0%; Score 550.5; DB 14; Length 485;
```



```
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, KYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2615
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2615
```

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Query Match 21.6%; Score 541.5; DB 15; Length 485;
Best Local Similarity 28.5%; Pred. No. 9.4e-37;
Matches 148; Conservative 94; Mismatches 176; Indels 101; Gaps 17;

QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCI-----TEHWYRQEAQAGARDCEPCR 54
DB 9 AIVEEVACPICMFTLREPSIDCGHSCFCHSLGLEIFGESQNW-----GYTCPLCR 61

QY 55 RTFAEPALAPSILANIVERYSSFFLDAILNARRAAPCOAH-DKVKLFCLTDRALLCF 113
DB 62 APVQPNLRPNQLANVVEKVRLLRLHPGMGLK-GDLCEHGEKLMKFKEDVLINCEA 119

QY 114 CDEPALHEQHVGTGDDAFDELQRELDQALQDSEREHTEALQLLKRQLAET-KSSTK 172
DB 120 CSQSPHEAHSVVPMEDEVAVYKWLHEALHLK-KEQEEAWKLEVGGERKRTATWKI 178

QY 173 SLRTTIGAEFERLHRLREROKAMLEELADTARTLTDIEQKVORYSQQLR-----KVQEG 228
DB 179 TRKQSVWFEFYQRLLLEKKQPPH-FOLGAEVAAALASIQREAAETMQKLELNHSELI 237

QY 229 AQLQERLAETDRHTELAGVASISERLKGKIHETNLTIEDFTPSKYTGPLQYTIWKS 288
DB 238 SQVLWRMIAB-----LKERSQRPVR-----W--MLQ 261

QY 289 DI-----HPVPAAL-----TLDPGTAHORLILSD 313
DB 262 DIQEVNRSKWSLQOPEPISLELTKDCRVLGLREILKTYAADVRLDPTATYSRLIVSE 321

QY 314 CTTIVAGNLHPQLOPSKPRFDEVSVLGSEAFSSGVHVEVVAEKTQWVIGLAHEAAS 373
DB 322 RKRWHYGDITN-QKLPDNPFRFYRINYVLGSCQTSRGRHYWEVEVGORSEWGLGVCKQ 380

QY 374 RKGSIOIQPSRGFYCVIMHDGNOYSACTEPWTRINVRDKLDKVGVDYDQGLLIYFNAD 433
DB 381 RKEVVLSPHYGFWVTLRKNERYRAGTDEYPLSLPVPVRRVGIFVDYEAHDSIFNVT 440

QY 434 DM-SWLYTF-REKPPGKLCYSFPGOSHANGKNVQLRI 470
DB 441 DCGSHIFTPFRYPFGRLLFPYFPCYS-IGTNTNAPLAI 478
```

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RESULT 9
US-10-104-047-3482
; Sequence 3482, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cdna
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3482
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3482

Query Match 20.0%; Score 501; DB 15; Length 471;
Best Local Similarity 29.4%; Pred. No. 2.3e-33;
Matches 143; Conservative 91; Mismatches 208; Indels 44; Gaps 14;

QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWYRQEAQAGARDCEPCTEAEPALA 63
DB 9 NLORESSCPICLEYLKDPTVINCNGHNFCHSCLSVSW--KDLDDTFFCPVCRFCFPYKSPR 66

QY 64 PSLKLANIVERYSSFFLDAILNARRAAP-----CQAHDK-VKLFCLTDRALLCFCD 115
DB 67 RNPQLNLTE-----IAQLQIRSKRKRQKENAMCEKHQNLTLFCVKDLLEILCTQCS 120

QY 116 EPALHEQHVGTGDDAFDELQRELDQALQDSEREHTEALQLLKRQLAETKSSTKSLR 175
DB 121 FSTKHQHYVICPIKKAASYHREBLEGSLEPLRNRIERVEKVILOQSKSVLKKVYEYKR 180

QY 176 TTIGAEFERLHRLREROKAMLEELADTARTLTDIEQKVORYSQQLRQVQGAQLQER 235
DB 181 BEINSEFEQIRFLQNEQEMILRQIDEMNILA-----KLNENLVELSDVSTLKH 233

QY 236 LAETDRHTELAGVASISERLKGKIHE-TNLTIED-----FPTSKEY--TGPLYTIWKS 289
DB 234 LREVEGKSVQSNLELLTQ-AKSMHHKYQNLKCPPELFSFRLTKYGFSLPPQYS---GLDRI 289

QY 290 IHPVPAALTLDPGTAHORLILSDCTIIVAGNLHPQLOPSKPRFDEVSVLGSEAFSSG 349
DB 290 IKPFQVDVILDNTAHPQLLVSEDRKAVRYERKKRNICYD-PRRFYVCPAVLGSRQFPSSG 348

QY 350 VHYVEVVAEKTQWVIGLAHEAASRKGSIQIOPS--RGFYCVIMHDGNOYSACTEPWTRL 407
DB 349 RHYWEVEGKPKWILGVQCDCLLR--NWQDQPSVLGGFWAIGRYMKSQVVASGPKTQL 406

QY 408 NVRDKLDKVGVDYDQGLLIIFYNADMSWLTFFREKFFKLCYSFPGOSHANGKNVQ 467
DB 407 LPWKPFSKIGIFLDYELGDLFSFNMNDRSILYTFNDCFTFAVWPYF-----YTGTDSEP 460

QY 468 LRINTV 473
DB 461 LKICSV 466

RESULT 10
US-10-104-047-3664
; Sequence 3664, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cdna
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
```

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; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3664
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3664

```

Query Match	20.0%;	Score 500;	DB 15;	Length 468;
Best Local Similarity	27.5%;	Pred. No. 2.8e-33;		
Matches 133;	Conservative 91;	Mismatches 212;	Indels 48;	Gaps 11;
QY	4	SLKDELLCSLCLSYQDPVSLGCEHYECRRCTTEHHWVQEAQAGARDCECERTEFAEALA	63	
Db	9	NRELETCFICLDYFSSPVITTECHGSLVCLLSRW--EEHNTPLSCPECWRTLEGPHFQ	66	
QY	64	PSUKLANIVERYSFFPDAILNARRARPCQAHDKVKLFCITDRALLCFFCDEPA----	118	
Db	67	SNERLGR-----ASIAQLRSQVLQSEDEQSGYGRMPTAKALSDDEQGSFAV	116	
QY	119	--LHEQCHQVTDIDAFDELORELKDQALQALQDSREHTEALQLLKRQIAETKSTKSLRT	176	
Db	117	AQSHGANRHLSSAEHREKLCQEIINLLRVRKKEAQAVLTHERKVKLCQEBTKCKQ	176	
QY	177	TIGEAPERLHLREERQKAMLEEELEADTARTLTIDIEKVQVYSQOLAKVQEGAILERL	236	
Db	177	VVTSEYMKHQFLKEEESQQLQLEQBEKENMRKLNRNEIKLTQOIRS-----LSKMI	229	
QY	237	ALDRHTFLAGVASLSERLKGKHET-----NLVYEDPPTSKYTGPLQYTIWKSLFQ	288	
Db	230	AQIESSSQSAFESL--EVRGALERSBPLLLQCEATTLSLCRIITG-----MKE	279	
QY	289	DIHPVPAALTLDPGTAHQRIILSDCTIVAYGNLHPQLODSPKRFVDVSVLGSFAPS	348	
Db	280	MLRKFSTEITLDPATANAYILVLEDLKSVMYGGSR--QQLPDNPERFQDSATVLGTQIFTS	338	
QY	349	GVHYWEVVAEKTQWIGLAHEAASRKGSIQIPSRGFYCIVMHGDGNQYSA--CTEPTWRL	407	
Db	339	GRHYWEVEVGKTEWEVGICKDSVSRKGNLPKPGDLFSLIGLKIGDGYSLWVSSPLKQG	398	
QY	408	NVRDKLDKVGFFLDYDGLLIFYNADMSWLYTF--REKFPCKLCSYFSPQOSHANGKNVQ	466	
Db	399	HVREPVCKVGFLDYESGHTAFNGTIDESLIFYFPQASFOEARLPITESCLPN--EGNTID	457	
QY	467	PLRI 470		
Db	458	PLTI 461		

```

RESULT 11
US-10-093-463-74
/ Sequence 74, Application US/10093463
/ Publication No. US20030208039A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Shenoy, Surash
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Pochart, Pascal
/ APPLICANT: Zhong, Mei
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Mezes, Peter
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Li, Li
/ APPLICANT: Zerkhusen, Bryan
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Vernet, Corinne

```

1	APPLICANT:	Pena, Carol
2	APPLICANT:	Burgess, Catherine
3	APPLICANT:	Liu, Xiaohong
4	APPLICANT:	Spytek, Kimberly
5	APPLICANT:	Gorman, Linda
6	APPLICANT:	Spaderna, Steven
7	APPLICANT:	Voss, Edward
8	APPLICANT:	Malyankar, Uriel
9	APPLICANT:	Anderson, David
10	APPLICANT:	Patturajan, Meera
11	APPLICANT:	Miller, Charles
12	APPLICANT:	Taupier, Raymond J. Jr.
13	TITLE OF INVENTION:	No. US20030208039A1el
14	TITLE OF INVENTION:	Encoding The Antigens
15	FILE REFERENCE:	21402-290A (Cura 590AT)
16	CURRENT APPLICATION NUMBER:	US/10/093,463
17	CURRENT FILING DATE:	2002-06-24
18	PRIOR APPLICATION NUMBER:	60/283,675
19	PRIOR FILING DATE:	2001-04-14
20	PRIOR APPLICATION NUMBER:	60/338,092
21	PRIOR FILING DATE:	2001-12-03
22	PRIOR APPLICATION NUMBER:	60/274,281
23	PRIOR FILING DATE:	2001-03-08
24	PRIOR APPLICATION NUMBER:	60/274,101
25	PRIOR FILING DATE:	2001-03-08
26	PRIOR APPLICATION NUMBER:	60/325,681
27	PRIOR FILING DATE:	2001-09-27
28	PRIOR APPLICATION NUMBER:	60/304,354
29	PRIOR FILING DATE:	2001-07-10
30	PRIOR APPLICATION NUMBER:	60/279,995
31	PRIOR FILING DATE:	2001-03-30
32	PRIOR APPLICATION NUMBER:	60/294,899
33	PRIOR FILING DATE:	2001-05-31
34	PRIOR APPLICATION NUMBER:	60/287,424
35	PRIOR FILING DATE:	2001-04-30
36	PRIOR APPLICATION NUMBER:	60/299,027
37	PRIOR FILING DATE:	2001-06-18
38	PRIOR APPLICATION NUMBER:	60/309,198
39	PRIOR FILING DATE:	2001-07-31
40	PRIOR APPLICATION NUMBER:	60/281,194
41	PRIOR FILING DATE:	2001-04-04
42	PRIOR APPLICATION NUMBER:	60/274,194
43	PRIOR FILING DATE:	2001-03-08
44	PRIOR APPLICATION NUMBER:	60/274,849
45	PRIOR FILING DATE:	2001-03-09
46	PRIOR APPLICATION NUMBER:	60/330,380
47	PRIOR FILING DATE:	2001-10-18
48	PRIOR APPLICATION NUMBER:	60/275,235
49	PRIOR FILING DATE:	2001-03-12
50	PRIOR APPLICATION NUMBER:	60/288,342
51	PRIOR FILING DATE:	2001-05-03
52	PRIOR APPLICATION NUMBER:	60/275,578
53	PRIOR FILING DATE:	2001-03-13
54	NUMBER OF SEQ ID NOS:	370
55	SOFTWARE:	PatentIn Ver. 2.1
56	SEQ ID NO 74	
57	LENGTH:	4675
58	TYPE:	PRT
59	ORGANISM:	Homo sapiens
60	US-10-093-463-74	

```

Query Match      19.9%; Score 499.5; DB 15; Length 4675;
Best Local Similarity 27.2%; Pred. No. 8.3e-32;
Matches 166; Conservative 68; Mismatches 187; Indels 189; Gaps 18;

QY      1  MACSLKDELLCSICLSIYQDPVSLGGEHVFRCRITTEHWVQBAQAGARDCECRRTPAEP 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4076 LSTNLQGEATCAICLDYFTDPVMTDGHNFCRRCIRRCWGQPE--GPYACPECKELSPQR 4133

QY      61  ALAPSLKLANIVERYSSFPDLAINARRARP-----CQAH-DKVKULFCLTDRALLCF 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4134 NLRPNRPFLAKMAEM-----ARRLHPSPVPGQVCPAHPREPLAAFCGDELRLICA 4182

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Qy	61	ALAPSLXLANIVERISSFPFLDAILNARRAAPCOAH-DKVKLFCTUDRALLGFFCDEPAL	119
Db	70	SLRKNKQLGSLIE-----ALKETDQMSCBEGHGFHLFCBDEGOLICWRCEAPQ	120
Qy	120	HEQHQVTGIDDAFDELOBELKDQIQALQDSREHTEALQLIKROLAETKSSYKSLRTTIG	179
Db	121	HKGHTTALVEDVCQYKEKQEAUTKQLEDRCTEQKLSMTAMRTKKWEKVOIQOKIR	180
Qy	180	EAPERLHRLREROKAMLEELAEADPARTLT--DIEQKVQVSQOQLR-----KVQBG	228
Db	181	SDFKNLQCFLHEEKSYLWRLEKEEQOQLSRLDYEAGLGSKNELKSHILELEKCCQS	240
Qy	229	AQILQERLAETDRHTFLAGVASLSERLKGKIHETNLTVEDPFTSKYTGDPLOTTIKWSLPQ	288
Db	241	AQKLLQNVDTI-----LSRSWAKLETSEAVSLHETMTCNVSKLYEDVKMKLRS	289
Qy	289	DIHPVPAALTLDPGTAHORLILSDCTIVAYGNLHPLOPLD-SPAREFVEVSVLGSEAFS	347
Db	290	--HQV--SVTLDPDTAHHELILSEDRRQVTRG--YTOENQDTSRRRFAFPCLVCGEGFT	343
Qy	348	SGVHYVEVVVAEKQTQWITGLAHEAASRKGSIQIPSRGFCYCYIMVDGNOYSACTEPWTKL	407
Db	344	SGRRYFEVDVGEIGCWDLGVCMENVQRGTGMKQEPQSGFWTLRLCKKGYVALTSPPTSL	403
Qy	408	NVRDKLDKGVFLDYDQGLLIFYNADDMWSLWYTF-REKFPGLKCSYF	453
Db	404	HLHROPILLVGTLFDYEAAGVSGFYNGTGHIEFTFPKASFDTLRPYF	450

RESULT 14

```

US-10-617-217A-97
; Sequence 97, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE OF INVENTION: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 97
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-97

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Query Match      19.6%; Score 492; DB 16; Length 465;
Best Local Similarity 29.3%; Pred. No. 1.3e-32;
Matches 137; Conservative 80; Mismatches 206; Indels 44; Gaps 11;

y      5 LKDELCTCLSIYQDPSVSGEHVFCRCRCITEHWVROEAQARD----CBECRRTAEP 60
      : : ||||| : : : : : : : : : : : : : : : : : : : : : : : :
c      10 MMEERATCSLSLMTNPVSINGHGYCHLCTIDFFKPNPQKLRQETFCPCQCRAPFMD 69
      : : ||||| : : : : : : : : : : : : : : : : : : : : : : : :
y      61 ALAPSLKIANIVERYSSFFLDAILNARRAAPQAH-DVKVLFCLTDRAILLCFCCDEPAL 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b      70 SLRPNKQLGSLIE-----ALKETQMSCEEHGQFHLFCDEGQLICWRCERAPQ 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
y      120 HQSQHVTGDDAFDELQRELKDQALQDSEHTEALQLLKQIAETKSSKTSILRTTIG 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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121 HKGHTTALVEDVCOQYKEKQLEAVTKLQLEDRCTEQKLSWTAMRTTKWEKVQIQOKIR 180
180 EAFERLHRLRLRQKAMLEELPADTARTLT--DIEQKVORYSQOLR-----KVQEG 228
181 SDFKNLCQCFLHEEKSYLWLEKEQOQLSLRLDYEAGLGKLSNELKSHILEEKCQGS 240
229 AQLIOERLAETDRHTFLAGVASILSERLKGKIHETNLTYEDFPTS KYTGPLOYTIWKS L FQ 288
241 AQKLLQNVNDT-----LSRWAVKLETSEAVSLELHTMCVSKLYFDVKQMLRS 289
289 DIHPVPAALTLDPGTAHQHRLILSDDDCTIIVAYGNLHPQLQD-SPKRFDEVSVSLGSEAFS 347
290 --HQV--SVTLDPDTAHHELLISDRRRQVTRG--YTOENQDTSRRRFTAPPCVLCGEFT 343
348 SGVHYEVVVVAEKTQWVIGLAHEAASRKSSIQIOPSRGFYCIVMHDGNCYSACTEPWTRL 407
344 SGRRYPEVDVGECTGWDLVGCMENVORGTGCKMOEPSQSGFWTLRLCKKKKGVAULTSPPTSL 403
408 NVDRKDLKVGVFLDYDQGLLIFFYNADDMSWLYTF-REKFFGKLCYSYF 453
404 HLHEQPLLVGIFLDYEAGVVSVFYNGTGGCHIFFPKASFSDTLRPFY 450

RESULT 15
US-10-024-298A-99
; Sequence 99, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JPO088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-99

```

```

Query Match      19.5%; Score 489; DB 14; Length 465;
Best Local Similarity 29.3%; Pred. M. 2.3e-32;
Matches 137; Conservative 79; Mismatches 207; Indels 44; Gaps 11;

5  LKDELLSCISLSIYQDPVSLGCEHYFRCRCITEHWVQEAQGARD---CPECRRTAEF 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
10 MNEEATCSICLSLMTNPVSIWNGHSYCHLCITDFKKNPSQQLRQETFCFCQCRAPHMD 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ALAPSLKLANIVERYSSPFLDAILNARRAARPCQAH-DKVKLFCGLTRALLCFFCDEPAL 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
70 SLRPNKQGLSLIE-----ALKETQDMSCEEHGQPHLFCDEGOLICWRCERAPQ 120

120 HFQHQVQTGIDDAFDLQRELDKQQLQALQDSREHTAEALQLLKRQLAETKSTKSLRTTIG 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 HKGHTTALVEDYCQGYKEKLAQVATKLQLEDCRTEQKLSLSTAMETKWKKEVQIQORQKIR 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
QY 180 EAFERLHRLREROKAMLELEADTARTLT--DIEQVQRYSQQLR-----KVOEG 228
Db 181 SDFANLOCFLHBEKSYLWLEKEEQTLKRLRDEAGLGKSNELKSHILEEERQGS 240
QY 229 AQILQERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFPPTSKYTGPLQYTIWKSLEFQ 288
Db 241 AQKLLQNVNT-----LSRSWAVKLETSEAVSLELHTMCNVSKLYFDVKMLRS 289
QY 289 DIHPVPAALTLDPGTAHORLILSDDCITIVAYGNLHPQLQD-SPKRFDFVEVSVLGSEAFS 347
Db 290 --HQV--SVTLDPDTAHHELILSEDRRQVTRG--YTOENQDTSRRRTAFPCVLGCEGFT 343
QY 348 SGVHYWEVVAEKTQWIGLAHERAASRKSGSIQIOPSRGEFCYIVMHDGNQYSACTEPWTRL 407
Db 344 SGRRYFEDVGEGTGWDLGVCMENVRGTGKQEPQSGFWTLRLCKKKGYVALTSPPTSL 403
QY 408 NVRDKLDKVGVLFDYDQGLLIFYNADDMSWLYTF-REKFPKGLCSYF 453
Db 404 HLHEQPLLVGIFLDYEAGVVSFYNGNTCCHIFTFPKASFSDTLRPYF 450
```

Search completed: July 23, 2004, 15:13:46
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:03:00 ; Search time 55 Seconds
(without alignments)
2440.183 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELLCSICLSIYQD.....GQSHANGKNVQPLRINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2504	100.0	475	5 AAU78657	AAU78657 Human tum
2	2504	100.0	475	7 ADC37269	ADC37269 Nuclear f
3	2491	99.5	475	4 AAB93138	AAB93138 Human pro
4	1983	79.2	394	7 ADC37455	ADC37455 Nuclear f
5	1312	52.4	304	5 AAU78658	AAU78658 Human tum
6	662.5	26.5	488	7 ADC37445	ADC37445 Nuclear f
7	634	25.3	123	4 AAM88857	AAM88857 Human imm
8	631	25.2	735	4 ABG26213	ABG26213 Novel hum
9	613	24.5	500	4 AAG89346	AAG89346 Human sec
10	583	23.3	513	7 ADC37447	ADC37447 Nuclear f
11	583	23.3	580	3 AAB43498	AAB43498 Human can
12	567	22.6	486	6 ABJ38678	ABJ38678 Human nuc
13	560	22.4	468	5 ABG97352	ABG97352 Human CGD
14	552.5	22.1	475	2 AAR15148	AAR15148 Ro/SSA au
15	550.5	22.0	485	5 AAM48396	AAM48396 Human SSA
16	550.5	22.0	485	5 ABP64866	ABP64866 Human pro
17	550.5	22.0	485	6 ABP55392	ABP55392 Human MDD
18	550.5	22.0	511	7 ADC37443	ADC37443 Nuclear f
19	541.5	21.6	485	6 ADA55047	ADA55047 Human pro
20	520	20.8	516	4 AAE02616	AAE02616 Murine ha
21	505.5	20.2	488	4 AAB95331	AAB95331 Human pro
22	501	20.0	471	7 ADB65328	ADB65328 Human pro
23	500	20.0	468	7 ADB65510	ADB65510 Human pro
24	499.5	19.9	4675	5 ABP70085	ABP70085 Human NOV
25	492	19.6	465	5 ABP61472	ABP61472 Human NF-

26	491	19.6	630	7	ADC37237	ADC37237 Nuclear f
27	489	19.5	465	2	AAW78921	AAW78921 Human hae
28	489	19.5	465	5	ABP61473	ABP61473 Human NF-
29	487	19.4	717	4	ABG21361	ABG21361 Novel hum
30	483	19.3	493	4	AAE02618	AAE02618 Human hae
31	483	19.3	504	4	AAE02617	AAE02617 Human hae
32	475.5	19.0	4691	5	ABP70084	ABP70084 Human NOV
33	458	18.3	477	3	AAB42919	AAB42919 Human ORF
34	449	17.9	539	6	ABU03730	ABU03730 Human exp
35	449	17.9	539	6	ABU03731	ABU03731 Human exp
36	449	17.9	539	6	ABU03729	ABU03729 Human exp
37	449	17.9	539	6	ABU03732	ABU03732 Human exp
38	438.5	17.5	545	7	ADC37235	ADC37235 Nuclear f
39	433.5	17.3	781	2	AAU09001	AAU09001 FMF assoc
40	427.5	17.1	781	5	AAO17853	AAO17853 Pryn dom
41	422.5	16.9	477	2	AAU01522	AAU01522 Human mar
42	418	16.7	475	3	AAAB29655	AAAB29655 Human mem
43	418	16.7	475	5	ABG79337	ABG79337 Human foe
44	418	16.7	475	6	ADA54825	ADA54825 Human pro
45	414.5	16.6	488	4	ABB50231	ABB50231 Human tra

ALIGNMENTS

RESULT 1
AAU78657
ID AAU78657 standard; protein; 475 AA.

XX AC AAU78657;
XX
XX
DT 18-JUN-2002 (first entry)
XX
XX
DE Human tumour suppressor CAR-1.
XX

Human; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
colon cancer; stomach cancer; breast cancer; endometrial cancer;
prostate cancer; testicular cancer; ovarian cancer; skin cancer;
head and neck cancer; oesophageal cancer; bone marrow cancer;
chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX
XX
EN WO200212285-A2.
XX
XX
PD 14-FEB-2002.
XX
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
XX
PR 10-AUG-2000; 2000US-0225033P.
PR 23-AUG-2000; 2000US-0227560P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
XX
PI Killary A, Chandler D, Lott S;
XX
XX
DR WPI; 2002-269088/31.
DR N-PSDB; ABK12806.
XX
XX
PS New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
diagnosing cancer, for altering the phenotype of a tumor cell, for
treating cancers or as a diagnostic or prognostic indicator of cancer.

Claim 23; Page 131-132; 185pp; English.

The invention relates to an isolated polynucleotide encoding a
polypeptide being tumour suppressor, CAR-1. Also included are fragments
of the polynucleotide from 15-5000 nucleotides, fragments of the protein
from 10-50 amino acids, an expression cassette comprising the
polynucleotide under the control of a promoter operable in eukaryotic
cells, a method for suppressing growth of a cancer cells by contacting
the cells with the expression cassette (i.e. gene therapy), a cell

CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1, or by
 CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (1p31-1p36). The present sequence represents human CAR-1
 CC
 XX
 SQ

Sequence 475 AA;

Query Match 100.0%; Score 2504; DB 5; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.3e-208;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 QY 61 ALAPSLKLANIVERYSSFPDLALNNARRAAPCOAHDKVKLFCLTDRLALCFFCDEPALH 120
 DB 61 ALAPSLKLANIVERYSSFPDLALNNARRAAPCOAHDKVKLFCLTDRLALCFFCDEPALH 120
 QY 121 EQHVTGIDDAFDELQRELDKQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 DB 121 EQHVTGIDDAFDELQRELDKQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 QY 181 APERLHRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVQEGAIQLQERLAETD 240
 DB 181 APERLHRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVQEGAIQLQERLAETD 240
 QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDIHPVPAALTLD 300
 DB 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDIHPVPAALTLD 300
 QY 301 PGTAHQRLILSDCTTIVAGNLHPQLQSPKRFDEVSVLGSEAFSSGVHYWEVVVAEK 360
 DB 301 PGTAHQRLILSDCTTIVAGNLHPQLQSPKRFDEVSVLGSEAFSSGVHYWEVVVAEK 360
 QY 361 TQWVIGLAHEAASRKGSIQIOPSRGFYCIVMHNGNYSACTEPWTRNLNRVDKLDKGVFL 420
 DB 361 TQWVIGLAHEAASRKGSIQIOPSRGFYCIVMHNGNYSACTEPWTRNLNRVDKLDKGVFL 420
 QY 421 DYDQGLLIIFYNADMSWLYTFREKFPKGLCSYFSPGSHANGKNVQPLRINTVRI 475
 DB 421 DYDQGLLIIFYNADMSWLYTFREKFPKGLCSYFSPGSHANGKNVQPLRINTVRI 475

RESULT 2

ADC37269

ID ADC37269 standard; protein; 475 AA.

XX
 AC ADC37269;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 102.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0336829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASahi KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI; 2003-505282/47.
 DR N-PSDB; ADC37268.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers, or
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 1; SEQ ID NO 102; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 475 AA;
 Query Match 100.0%; Score 2504; DB 7; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.3e-208;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCECRRTFAEP 60
 QY 61 ALAPSLKLANIVERYSSFPDLALNNARRAAPCOAHDKVKLFCLTDRLALCFFCDEPALH 120
 DB 61 ALAPSLKLANIVERYSSFPDLALNNARRAAPCOAHDKVKLFCLTDRLALCFFCDEPALH 120
 QY 121 EQHVTGIDDAFDELQRELDKQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 DB 121 EQHVTGIDDAFDELQRELDKQALQDSEHTEALQLLKRLAETKSKSLRTTIGE 180
 QY 181 APERLHRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVQEGAIQLQERLAETD 240
 DB 181 APERLHRLREROKAMLELEADTARTLTDIEOKVORYSQOLRKVQEGAIQLQERLAETD 240
 QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDIHPVPAALTLD 300
 DB 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGPLQYTIWKSIFQDIHPVPAALTLD 300

QY 301 PCTAHORLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYVEVVVAEK 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 PCTAHORLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYVEVVVAEK 360
QY 361 TQWVIGLAHEAASRKSGSIQIQPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TQWVIGLAHEAASRKSGSIQIQPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
QY 421 DYDQGLLIFYNADDMMSWLYTFREKFPKLCYSYSPGQSHANGKNVQPLRINTVRI 475
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 DYDQGLLIFYNADDMMSWLYTFREKFPKLCYSYSPGQSHANGKNVQPLRINTVRI 475

RESULT 3
AAB93138
ID AAB93138 standard; protein; 475 AA.
AC AAB93138;
XX
XX 26-JUN-2001 (first entry)
DT Human protein sequence SEQ ID NO:12037.
DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.
KW Homo sapiens.
OS
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID NO 12037; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC oligonucleotides, all of which are used in the exemplification of the present invention
XX
SQ Sequence 475 AA;
Query Match 99.5%; Score 2491; DB 4; Length 475;
Best Local Similarity 99.6%; Pred. No. 3.1e-207;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MACSLDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQBAQGARDCECRRTPAEP 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MACSLDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQBAQGARDCECRRTPAEP 60
QY 61 ALAPSLKLANIVERYSSFPDLAINARRARPCQAHDKVLCITDRAALLCFCDEPALH 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 ALAPSLKLANIVERYSSFPDLAINARRARPCQAHDKVLCITDRAALLCFCDEPALH 120
QY 121 EQHOVTGIDDAFDELORELKQDQALQDSREHTEALQLLKQLAETKSKSLRTTIGE 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 EQHOVTGIDDAFDELORELKQDQALQDSREHTEALQLLKQLAETKSKSLRTTIGE 180
QY 181 AFERLHRLLEERQKAMLELEADTARTLTDEOKVQRYSQLRKVQEGAQILOERLAETD 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AFERLHRLLEERQKAMLELEADTARTLTDEOKVQRYSQLRKVQEGAQILOERLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGLOVYTIWKSFLQDTHPVAALTLD 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 RHTFLAGVASLSERLKGKIHETNLTYEDFPTSKYTGLOVYTIWKSFLQDTHPVAALTLD 300
QY 301 PGTAHORLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYVEVVVAEK 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 PGTAHORLILSDCTTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYVEVVVAEK 360
QY 361 TQWVIGLAHEAASRKSGSIQIQPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 TQWVIGLAHEAASRKSGSIQIQPSRGFYCIYVMDGNQYSACTEPWTRLNVRDKLDKVGVL 420
QY 421 DYDQGLLIFYNADDMMSWLYTFREKFPKLCYSYSPGQSHANGKNVQPLRINTVRI 475
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 DYDQGLLIFYNADDMMSWLYTFREKFPKLCYSYSPGQSHANGKNVQPLRINTVRI 475

RESULT 4
ADC37455
ID ADC37455 standard; protein; 394 AA.
XX
XX ADC37455;
XX
XX 18-DEC-2003 (first entry)
XX
XX Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 288.
DE
XX Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
KW cancer; infectious disease; bone disease; AIDS;
KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human.
XX
XX Homo sapiens.
XX
XX W02003048202-A2.
XX
XX 12-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-JP012644.
PF
XX 03-DEC-2001; 2001JP-00368692.
PR 05-DEC-2001; 2001US-0335829P.
PR 03-OCT-2002; 2002JP-00291302.
PR 04-OCT-2002; 2002US-0415769P.
XX
XX (ASAH) ASAH KASEI KK.
PA
XX

```

PI Matsuda A, Muramatsu S;
XX
DR WPI; 2003-505282/47.
XX N-PSDB; ADC37454.
XX
XX New purified protein that activates nuclear factor kappa B (NF-kappaB),
PT useful for treating inflammation, autoimmune diseases, cancers,
PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
PT ischemic disorders.
XX
XX Claim 1; SEQ ID NO 288; 938pp; English.
PS
XX The present invention relates to novel proteins and their coding
XX sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
CC kappaB). The proteins and their coding sequences are useful for treating
CC a disease associated with NF-kappaB activation, such as inflammation,
CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
CC neurodegenerative diseases, or ischaemic disorders.
XX
XX Sequence 394 AA;
PS
Query Match 79.2%; Score 1393; DB 7; Length 394;
Best Local Similarity 100.0%; Pred. No. 3e-163;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
OY 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCOAHDKVKLFCLTDRALLCFFCDEPALH 120
DB 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCOAHDKVKLFCLTDRALLCFFCDEPALH 120
OY 121 EQHQTGDDAFDELQRELKQQLQALQDSREHTEALQKQLAETKSSKSLTTTIGE 180
DB 121 EQHQTGDDAFDELQRELKQQLQALQDSREHTEALQKQLAETKSSKSLTTTIGE 180
OY 181 APERLHRLLRKAMLELEADTARTLTDEQKVQRYSQQLRVQEGAILQERLAETD 240
DB 181 APERLHRLLRKAMLELEADTARTLTDEQKVQRYSQQLRVQEGAILQERLAETD 240
OY 241 RHTFLAGVASLSEKLGKHETNLTYEDPPTSKYTGPLQYTIWKSFLQDIHPVPAALTLD 300
DB 241 RHTFLAGVASLSEKLGKHETNLTYEDPPTSKYTGPLQYTIWKSFLQDIHPVPAALTLD 300
OY 301 PCTAHORLILSDDCITIVAYGNLHPQLODSPKRPDEVEVSLGSEAFSSGVHYWEVVAEK 360
DB 301 PCTAHORLILSDDCITIVAYGNLHPQLODSPKRPDEVEVSLGSEAFSSGVHYWEVVAEK 360
OY 361 TQWVIGLAHEAASRKGSIQIQ 381
DB 361 TQWVIGLAHEAASRKGSIQIQ 381
RESULT 5
AAU78658
ID AAU78658 standard; protein; 304 AA.
XX
AC AAU78658;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human tumour suppressor CAR-1 produced by alternative splicing.
XX
XX Human; tumour suppressor; CAR-1; cytostatic; cancer; tumour;
KW gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer;
KW colon cancer; stomach cancer; breast cancer; endometrial cancer;
KW prostate cancer; testicular cancer; ovarian cancer; skin cancer;
KW head and neck cancer; oesophageal cancer; bone marrow cancer;
KW chromosome 1p31-1p36.
XX
XX Homo sapiens.
OS
XX

```

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PN WO200212285-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025269.
XX
PR 10-AUG-2000; 2000US-0225033p.
XX
PR 23-AUG-2000; 2000US-0227560p.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Killary A, Chandler D, Lott S;
PI
XX WPI; 2002-269088/31.
DR
XX New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for
PT diagnosing cancer, for altering the phenotype of a tumor cell, for
PT treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
XX Claim 23; Page 133; 185pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
CC from 10-50 amino acids, an expression cassette comprising the
CC polynucleotide under the control of a promoter operable in eukaryotic
CC cells, a method for suppressing growth of a cancer cells by contacting
CC the cells with the expression cassette (i.e. gene therapy), a cell
CC comprising the expression cassette, an anti-CAR-1 monoclonal or
CC polyclonal antibody, a hybridoma cell that produces the monoclonal
CC antibody, a method of diagnosing a cancer by assessing the expression of
CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject;
CC methods for altering the phenotype of a tumour cell, methods for treating
CC a subject with cancer by administering the tumour suppressor CAR-1, or by
CC administering a nucleic acid encoding the tumour suppressor CAR-1 and a
CC promoter active in eukaryotic cells, where the promoter is operably
CC linked to the region encoding the tumour suppressor, a non-human
CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
CC non-transgenic eukaryote, a method of screening a candidate substance for
CC anti-tumour activity by contacting a cell lacking functional CAR-1
CC polypeptide, with a candidate substance and determining the effect of the
CC candidate substance on the cell, an anti-tumour composition produced by
CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
CC substance, determining the effect of the candidate substance on the cell,
CC identifying a candidate inhibitor substance, and making a composition and
CC an isolated and purified nucleic acid that hybridizes, under high
CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
CC altering the phenotype of a tumour cell, for treating cancers (e.g.
CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
CC other tissues), and as a diagnostic or prognostic indicator of cancer.
CC CAR-1 may also be used in screening compounds for activity in either
CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
CC chromosome 1 (1p31-1p36). The present sequence represents a variant human
CC CAR-1 produced by alternative splicing of the CAR-1 cDNA
XX
XX Sequence 304 AA;
XX
Query Match 52.4%; Score 1312; DB 5; Length 304;
Best Local Similarity 91.8%; Pred. No. 3.8e-105;
Matches 257; Conservative 2; Mismatches 5; Indels 16; Gaps 1;
OY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWVQEAQAGARDCECRRTFAEP 60
OY 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCOAHDKVKLFCLTDRALLCFFCDEPALH 120
DB 61 ALAPSLKLANIVERYSSFFPLDAILNARRAAPCOAHDKVKLFCLTDRALLCFFCDEPALH 120

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PR	14-AUG-2000;	2000US-0224518P.
PR	14-AUG-2000;	2000US-0224519P.
PR	14-AUG-2000;	2000US-0225213P.
PR	14-AUG-2000;	2000US-0225214P.
PR	14-AUG-2000;	2000US-0225266P.
PR	14-AUG-2000;	2000US-0225267P.
PR	14-AUG-2000;	2000US-0225268P.
PR	14-AUG-2000;	2000US-0225270P.
PR	14-AUG-2000;	2000US-0225447P.
PR	14-AUG-2000;	2000US-0225577P.
PR	14-AUG-2000;	2000US-0225758P.
PR	14-AUG-2000;	2000US-0225759P.
PR	18-AUG-2000;	2000US-0226279P.
PR	22-AUG-2000;	2000US-0226681P.
PR	22-AUG-2000;	2000US-0226686P.
PR	22-AUG-2000;	2000US-0227182P.
PR	23-AUG-2000;	2000US-0227009P.
PR	30-AUG-2000;	2000US-0228924P.
PR	01-SEP-2000;	2000US-0229287P.
PR	01-SEP-2000;	2000US-0229343P.
PR	01-SEP-2000;	2000US-0229344P.
PR	01-SEP-2000;	2000US-0229345P.
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PR	05-SEP-2000;	2000US-0229513P.
PR	06-SEP-2000;	2000US-0230437P.
PR	06-SEP-2000;	2000US-0230438P.
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PR	14-SEP-2000;	2000US-0232400P.
PR	14-SEP-2000;	2000US-0232401P.
PR	14-SEP-2000;	2000US-0233063P.
PR	14-SEP-2000;	2000US-0233064P.
PR	14-SEP-2000;	2000US-0233065P.
PR	21-SEP-2000;	2000US-0234223P.
PR	21-SEP-2000;	2000US-0234274P.
PR	25-SEP-2000;	2000US-0234997P.
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PR	26-SEP-2000;	2000US-0235484P.
PR	27-SEP-2000;	2000US-0235834P.
PR	27-SEP-2000;	2000US-0235836P.
PR	29-SEP-2000;	2000US-0236327P.
PR	29-SEP-2000;	2000US-0236367P.
PR	29-SEP-2000;	2000US-0236368P.
PR	29-SEP-2000;	2000US-0236369P.
PR	29-SEP-2000;	2000US-0236370P.
PR	02-OCT-2000;	2000US-0236802P.
PR	02-OCT-2000;	2000US-0237037P.
PR	02-OCT-2000;	2000US-0237038P.
PR	02-OCT-2000;	2000US-0237039P.
PR	02-OCT-2000;	2000US-0237040P.
PR	13-OCT-2000;	2000US-0239935P.
PR	13-OCT-2000;	2000US-0239937P.
PR	20-OCT-2000;	2000US-0240960P.
PR	20-OCT-2000;	2000US-0241221P.
PR	20-OCT-2000;	2000US-0241785P.
PR	20-OCT-2000;	2000US-0241786P.
PR	20-OCT-2000;	2000US-0241787P.
PR	20-OCT-2000;	2000US-0241808P.
PR	20-OCT-2000;	2000US-0241809P.
PR	20-OCT-2000;	2000US-0241826P.
PR	03-NOV-2000;	2000US-0244617P.
PR	08-NOV-2000;	2000US-0246474P.
PR	08-NOV-2000;	2000US-0246475P.
PR	08-NOV-2000;	2000US-0246476P.
PR	08-NOV-2000;	2000US-0246477P.
PR	08-NOV-2000;	2000US-0246478P.
PR	08-NOV-2000;	2000US-0246523P.
PR	08-NOV-2000;	2000US-0246524P.
PR	08-NOV-2000;	2000US-0246525P.
PR	08-NOV-2000;	2000US-0246526P.
PR	08-NOV-2000;	2000US-0246527P.
PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
PR	08-NOV-2000;	2000US-0246609P.
PR	08-NOV-2000;	2000US-0246610P.
PR	08-NOV-2000;	2000US-0246611P.
PR	08-NOV-2000;	2000US-0246613P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
PR	17-NOV-2000;	2000US-0249209P.
PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-200	

CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 123 AA;
Query Match 25.3%; Score 634; DB 4; Length 123;
Best Local Similarity 96.7%; Pred. No. 7.2e-47;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 288 QDIHPVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFS 347
Db 3 RDEHPVPAALTLDPGTAHQRLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFS 62
QY 348 SGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIPSRGFCYIVMHDGNOYSACTEPTRL 407
Db 63 SGVHYWEVVAEKTQWVIGLAHEAASRKGSIQIPSRGFCYIVMHDGNOYSACTEPTRL 122
QY 408 N 408
Db 123 N 123
RESULT 8
ABG26213
ID ABG26213 standard; protein; 735 AA.
XX
AC ABG26213;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26204.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS90400.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 56572; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 735 AA;
Query Match 25.2%; Score 631; DB 4; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 168 KSSTKSLRTTIGEAFLRLRLRERQKAMLEELADTARTLTDIEQVRSQQLRKVQE 227
Db 598 KSSTKSLRTTIGEAFLRLRLRERQKAMLEELADTARTLTDIEQVRSQQLRKVQE 657
QY 228 GAQILQERLAETDRHTFLAGVASLSERLKGKIHTNLTIEDPPTSKYTGPIQYTIWKSLE 287
Db 658 GAQILQERLAETDRHTFLAGVASLSERLKGKIHTNLTIEDPPTSKYTGPIQYTIWKSLE 717
QY 288 QDIHP 292
Db 718 QDIHP 722
RESULT 9
AAG89346
ID AAG89346 standard; protein; 500 AA.
XX
AC AAG89346;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 466.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.
XX
OS Homo sapiens.
XX
PN W0200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-IB001938.
XX
PR 08-DEC-1999; 99US-0169629P.
PR 06-MAR-2000; 2000US-0187470P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
DR WPI; 2001-367870/38.
DR N-PSDB; AAG64949.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases.
XX
PS Claim 21; Page 913-914; 921pp; English.
XX
CC The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased
CC gene expression by rectifying mutations or deletions in a patient's
CC genome that affect the activity of GENSET or by supplementing the
CC patients own production of GENSET polypeptides. Conversely, antisense

Job time : 57 secs

```
XX 12-MAR-2001; 2001WO-FR000725.
XX
XX 17-MAY-2000; 2000FR-00006315.
XX
XX (ISTA-) ISTAC.
XX (INSP ) INST PASTEUR LILLE.
XX
XX Bahr G, Cocude C, Capron A;
XX
XX WPI; 2002-066692/09.
XX N-PSDB; ABA98677.
XX
XX New human Ro/SSA-like polypeptide, useful for treatment, prevention and
XX diagnosis of e.g. autoimmune disease and viral infection, also related
XX nucleic acid and antibodies.
XX
XX Claim 1; Page 86-88; 109pp; French.
XX
XX The present sequence is a novel human Ro/SSA-like protein, SSA-56 kDa.
XX The coding sequence for SSA-56 protein can be used for the diagnosis or
XX monitoring of autoimmune diseases (particularly systemic lupus
XX erythematosus, SLE, or Sjogren syndrome), infections by RNA viruses
XX (particularly HIV or hepatitis B and C) or chronic pathogen infections
XX associated with autoimmune manifestations. The coding sequence for SSA-56
XX protein can also be used to generate transgenic animals for studying the
XX aetiology of Ro/SSA-like protein-related diseases or effects of viral
XX infection on expression of Ro/SSA-like protein
XX
XX Sequence 485 AA;
XX
Query Match 22.0%; Score 550.5; DB 5; Length 485;
Best Local Similarity 29.3%; Pred. No. 1e-38;
Matches 150; Conservative 94; Mismatches 181; Indels 87; Gaps 17;
QY 4 SLKDELLCSICLSIYQDPVGLGCEHYFCRCRCITEHW-VRQEAQG-ARDQECRRTEFAEPA 61
Db 9 AIVEEVACPICTFIREPMSIDCGSFCHSGLWEIPGESQNWGYTCPLCRAPVQPRN 68
QY 62 LAPSLKLANIVERYSSFPDLAINARRAAPCOAH-DKVKLFCLTDRALLCFFCDEPAIH 120
Db 69 LRPNQLANVVEKVLRLHPGMGLK--GDLCEHGEKLMFKCKEDVLIMCEACSQSPRH 126
QY 121 EHQVTGIDDAFDELQRELKQLOALQDSERHTEALQLKQLAET-KSSTKSLRTTIG 179
Db 127 EAHSVPMEDVAVWEYKWEHLEHLK-KQSEAWKLEVGERRKRTATWKIQVETRKQSIY 185
QY 180 EAFERHLRLRRQKAMLEELADTARTLTIDIEQKVQYSQQLR----KVQEGAQLQER 235
Db 186 WEFEKYQRLLEKKQPPH-RQLGAEVAALASLOREAAETMQKLELNHSELIOQSQVLWRM 244
QY 236 LAETDRHTFLAGVSLSERLKGKIHETNLTIEDFTPTSKYTGPLQYTIWKSLEFQDI----- 290
Db 245 IAE-----LKERSQRPVR-----W--MLQDIQEVLN 268
QY 291 -----HPVPAAL-----TLDPGTAHORLILSDCTIVAYG 320
Db 269 RSKSWSLQOPEPISLELTKDQVGLREILKTYAADVRLDPTAYSRLLIVSDRKRVHYG 328
QY 321 NLHPQLQDSPKRFVDESVLGEAFSSGVHYWVWVAEKTQWVIGLAHEAASRKGSIQI 380
Db 329 DTN-QKLDPNPERFYRNIVLSQCISGRHYWEVVGDRSEWGLGVCKQNVDRKEVVYL 387
QY 381 QPSRFGYCIWMDGNGQYSACTEPWRLNVDRKLDKGVFLDYDQGLLIIFYNADDM-SWLY 439
Db 388 SPHYGFVIRLRKNGEYRAGTDEYFILSLPVPFRPVGFVDYEAHDIISFYNTDYGSHIF 447
QY 440 TF-REKFGKLCISYSPGOSHANGKNVQPLRI 470
Db 448 TFRYPFPGRLLPYFSPCYIS-ICTNNTAPLAI 478
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Search completed: July 23, 2004, 15:06:47

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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:05:45 ; Search time 19 seconds
(without alignments)
1290.649 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLKDELLCSICLSIYOD.....GQSHANGKNVQLINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	546.5	21.8	487	2	US-08-724-394A-7
2	486	19.4	485	2	US-08-724-394A-8
3	427.5	17.1	781	4	US-09-486-147-3
4	421	16.8	179	4	US-09-486-147-38
5	396	15.8	178	4	US-09-486-147-37
6	364.5	14.6	413	4	US-09-663-600A-198
7	348	13.9	183	4	US-09-486-147-36
8	339	13.5	584	4	US-09-910-174B-16
9	339	13.5	584	4	US-09-620-461-16
10	335.5	13.4	184	4	US-09-486-147-35
11	329	13.1	513	4	US-09-910-174B-18
12	329	13.1	513	4	US-09-620-461-18
13	321	12.8	610	2	US-08-724-394A-5
14	316.5	12.6	527	4	US-09-910-174B-10
15	316.5	12.6	527	4	US-09-620-461-10
16	315.5	12.6	529	4	US-09-910-174B-13
17	315.5	12.6	529	4	US-09-620-461-13
18	312.5	12.5	181	4	US-09-486-147-5
19	311.5	12.4	174	4	US-09-486-147-41
20	307.5	12.3	523	4	US-09-910-174B-11
21	307.5	12.3	523	4	US-09-620-461-11
22	305.5	12.2	540	2	US-08-724-394A-4
23	303	12.1	185	4	US-09-486-147-39
24	299	11.9	581	2	US-08-724-394A-2
25	295.5	11.8	581	2	US-08-724-394A-3
26	293	11.7	526	4	US-09-910-174B-9
27	293	11.7	526	4	US-09-620-461-9

Sequence 15, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 6, Appl
Sequence 171, Appl
Sequence 5, Appl
Sequence 43, Appl
Sequence 104, Appl
Sequence 5, Appl
Sequence 40, Appl
Sequence 42, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 44, Appl
Sequence 4209, Ap
Sequence 468, App
Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-724-394A-7
; Sequence 7, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF INVENTION: Sequences and Antibodies Thereto
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..487
OTHER INFORMATION: /note= "52 kD Ro"

US-08-724-394A-7

ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..485
OTHER INFORMATION: /note= "RoRet"
US-08-724-394A-8

Query Match 19.4%; Score 486; DB 2; Length 485;
Best Local Similarity 29.3%; Pred. No. 2.5e-37;
Matches 137; Conservative 80; Mismatches 213; Indels 38; Gaps 12;

QY 5 LKDELLCSICLSIYQDPVSLGCHYFCRCITTEHWVROEAQAGARD-----CPECRRFAEP 60
DB 10 MMEATCSICLSIMINPVINGCHSYCHLCITDFFKNPSQKQLROFTCCQCRAPFHM 69
QY 61 ALAPSLKLANIYERYSFPDLALNARRAAPCOAH-DKVKLFLCLTDRLALCFPCDEPAL 119
DB 70 SLRPNKQLSLIEALKE--TDQEMXXXXXXSCSEEGEQHLECEDEGQLICWRCEAPQ 127
QY 120 HEHQVGTGDDAFDELQRELKQLOALQDSEREHTEALQLLKQLAETKSTKSLRTTIG 179
DB 128 HKGHTTALVEDVCOGYKEKQAVTKLQLEDRECTEQLKSTAMRITKWEKVQIQOKIR 187
QY 180 EAFERLRLRERQKAMLEBELEADTARTLT---DIEQVORYSQQLR-----KVQEG 228
DB 188 SDFKNLQCFLEHEBEKSYLWLEKEBOQTLRLRDYEAGLGLKSNELKSHILEEKKQGS 247
QY 229 AQILQERLAETDRHTFLAGVASLSERLKGKHETNLTYEDFPTSKYTGPIQYTIWKSFLQ 288
DB 248 AQKLLQNVNDT-----LSRWAVKLETSEAVSLELHTMCNVSKLYFDVKWMLRS 296
QY 289 DIHPVPAALTDPCTAHQRLILSDDCCTIVAYGNLHPQLOPQD-SPKRPDVEVSLGSEAFS 347
DB 297 --HQV--SVTLDPDTHAHHELILSEDRQVTRG--YTQENQDTSRRRTAFPCVLGCEGFT 350
QY 348 SGVHYEVVVAEKTQWVIGLAHEAASRKSIGIQPSGFGYCIYVMDGNQYSACTEPWTFRL 407
DB 351 SGRRYFEVDVGEGTGMDLGVCMENVQRTGKMQPQSGFWTLRLCKKKGYVALTSPTSL 410
QY 408 NVRDKLKGVFLDYDQGLLIFYNADDMWS-WLYTF-REKFPGLKCSYF 453
DB 411 HLHEQPLVLGFLDYEAGVSVFYNGXNTGCHIFTFKASFSDTLRPYF 458

RESULT 3
US-09-486-147-3
Sequence 3, Application US/09486147
Patent No. 6627745
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as
APPLICANT: represented by the Secretary, Department of Health and Human
APPLICANT: Services
APPLICANT: Daniel L. Kastner
APPLICANT: Ivona Aksentijevich
APPLICANT: Michael Centola
APPLICANT: Zuoming Deng
APPLICANT: Raman Sood
APPLICANT: Francis S. Collins
APPLICANT: Trevor Blake
APPLICANT: P. Paul Liu

Query Match 21.8%; Score 546.5; DB 2; Length 487;
Best Local Similarity 30.4%; Pred. No. 4.7e-43;
Matches 150; Conservative 92; Mismatches 202; Indels 49; Gaps 16;

QY 7 DELICSLISYQDPVSLGCHYFCRCITTEHWVROEAQAGARD-----CPECRRTF 57
DB 12 BEVTCPICLDPFVEPVSTEGCHSGFQECIS-----QVGKGGGXXXXXXVCPVCRORF 66
QY 58 AEPALPSLKLANIYERYSFPDLALNARRAAPCOAH-DKVKLFLCLTDRLALCFPCDE 116
DB 67 LKLNLRPNRQLANVNNLKEISQEA--REGTOGERCAVHGERLHLFCEDKQKALCWVCAQ 124
QY 117 PALHEHQHVTGDDAFDELQRELKQLOALQDSEREHTEALQJ---LKQLAETKSTKYS 173
DB 125 SKRHRDAMVPLEEAAQEQYKQLQVALGELR-RKQELAEKLEVEIAIKR--ADWKKTVET 181
QY 174 LATTIGEAFERLRLRERQKAMLEBELEADTARTLTDBOKVORYSQQLRKVQEGAQIILQ 233
DB 182 QKSRHAEPVQKNFLVEEQQQLQLEKDERQRLIGKEKAKLAQO-----SQALQ 234
QY 234 ERLAETDRHTFLAGVASLSERL-----KGKHETNLTYEDFPTSKYTGPIQYTIWKS 286
DB 235 ELISELDRCHSALELLEQVIVLERSSEWNLKDLDTSPELRSVCHV-PXXXXGLKKM 293
QY 287 FQD--IHPVPAALTDPCTAHQRLILSDDCCTIVAYGNLHPQLOPQDSPKRPDVEVSLGSE 344
DB 294 LRTCAVH-----ITLDPDTANPWLILSEDRQVRLGDTQ-QSIPGNEERFDSYPMVLGAQ 347
QY 345 AFSSGVHYEVVVAEKTQWVIGLAHEAASRKSIGIQPSRFGYCIYVMDGNQYSACTEPW 404
DB 348 HFHSGKHVEVDVTKGEAWDLGVCRDSVRKKGHLLSSKSGFWTIWLNKQKYEAGTYQ 407
QY 405 TRLNVRDKLVGVFLDYDQGLLIFYN-ADDMWSLYTFRE-KFPGLKCSYFSPGQSHANG 452
DB 408 TPLHLQVPCQGVIFLDYAGWVSFYNTDHSGLIYSFSFCACTGRLRPFSPG-FNDGG 456
QY 463 KNQQLRINTVRI 475
DB 467 KNTAPLTLCPLNI 479

RESULT 2
US-08-724-394A-8
Sequence 8, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchibashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536

```

; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Rieke
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
; FILE REFERENCE: 14014.0314U1
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 781
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
US-09-486-147-3

Query Match      17.1%; Score 427.5; DB 4; Length 781;
Best Local Similarity 25.2%; Pred. No. 1.8e-31;
Matches 132; Conservative 79; Mismatches 168; Indels 145; Gaps 17;

QY 20 DPVSLGCEHYFCR--RCITETHWVQEAGQARD--CPECRRTF---APFALAPSLKLANIV 72
Db 321 DPVDGTCVRSCSPPEAVSGH---PQASGSGSPGRCQDSHERKSPGSLSPQ----- 370
QY 73 ERYSSFFPLDALINARRAARPCQAHDK--VKLFCLUTDRALLCFFCDPEALHEOHVTCIDD 130
Db 371 -----PLP-----QCKRLKQVQLLFCEHDDEPCLICLSQEHQGHKVRPIEE 414
QY 131 AFDELQELKDQALQDSREHTEALQLKQLAETKS-----STKSLRTTIGEAFERL 185
Db 415 VALEHKKKIQKLEHLKLRKSGEE-----QRSYGEKAVSFLKQTEALKQVRQKLEQV 469
QY 186 HRLRLRERQ-----KAMLEHELEAETAR----- 206
Db 470 YFLEQOEHEFVASLEDVGOMVGQIRKAYDTRVSDQIALDLALIGELEKECQSEWELLQ 529
QY 207 -----TLTDIEQKVQRYSQOLRKVQSGAQLQERLAETDRHTFLAG 247
Db 530 DIGDILHRAKTVVPPEKWTTPQELKQIKQLLHQKSEFEVKSTKVFSETL-RSEWMP--- 585
QY 248 VASLSERLKGKIHETNUTYEDFPSTKYTGPLQVTIMKSLPQDHPVPAALTDPGTAHQ 307
Db 586 --NVPELIGAQAHAVN-----VILDAETAYPN 610
QY 308 LIISDDCTIVAYGNLHPQPLQDSPKRFDVEVSVLGSEAFSSGVHYHVVAEKTQWIGL 367
Db 611 LIFSDDLKSVRLGNKW--ERLPDGPQRPDSCIIIVLGSFSLSGRYEVEVEGDKTAWILGA 669
QY 368 AHEAASRKSGSIQPSRGFFCIVMHDGNQYSACTEPTWRLNVRDKLDKVGVEVDYDQGLL 427
Db 670 CKTSISRKGNTWLSPENGYHVVIMMENEYQASVPTLLIKEPKRGVIFVDYRVGSI 729
QY 428 IFYNADMSWLYTFRE-KFPGKLCYSFSPGQSHANGKNVQPLRI 470
Db 730 SFYNVTARSHIYTFASCSFSGPLQIFSPG-TRDGGKNTAPLII 772

RESULT 4
US-09-486-147-38
; Sequence 38, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner

```

QY 60 PALAPSLKLANIVERYSSFFPILDAILNARRAARPCOAH-DKVKLFCLTDRALLCFPCDEPA 118
Db 66 EHLQANQHLANIVRELKEVKLSPDNGKKRDL--CDHGEKLLLFCKEDRKVICWLCERSQ 123
QY 119 LHEQHVTGIDDAFDELQRELKQALQDSREHTEALQILKRLAETKSTK-----SL 174
Db 124 EHRGHHTVLTREVFKECEKQLQAVLRLKKEBEE---AEKLEADIREKTSWKYQVQPE 179
QY 175 RTTIGEAERLHRLRERQKAMLELEADTARTLTDIEQKVQRYSQLRKVQOE----- 227
Db 180 RQRIQTEFDQRSILNNEEERELQRELBEEKTKOKFAEDELVOQKQVRELSDVBC 239
QY 228 -----GAQILQERLAETDRHTFLAGVASLSE--RLKKGKIHETNLTYEDPFTSKYGPLOY 280
Db 240 RQWSTMELLQD-----MSGIMKWSIWLK-----KPKMWSKKLKTVFHAPDLRSR 285
QY 281 TIWKSIFQDIHVPV---AALTIDPGTAHORLLISDDCTTIVAYGNLHPQLQDSPKRFDVE 337
Db 286 ML--QMFRELTAVRCVWVDVTLNVLNLNLVLSEDRQVIVSVPWPFQYN----- 335
QY 338 VSVLGSEAFSSGVHYWEVVAEKTQWVIG-----LAHEAASRKG-SIQIOPSR 384
Db 336 YGVLSGQYFSSGKHWEVDVSKTAMILGVCTYSRHMKYVVRRCANRONLYTKYRPLF 395
QY 385 GFYCIVMHDGNOYSA 399
Db 396 GYVIGLQNKCKYGA 410

RESULT 7
US-09-486-147-36
; Sequence 36, Application US/09486147
; Patent No. 6627745
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary, Department of Health and Human
; APPLICANT: Services
; APPLICANT: Daniel L. Kastner
; APPLICANT: Ivona Aksentijevich
; APPLICANT: Michael Centola
; APPLICANT: Zuoming Deng
; APPLICANT: Raman Sood
; APPLICANT: Francis S. Collins
; APPLICANT: Trevor Blake
; APPLICANT: P. Paul Liu
; APPLICANT: Deborah Gumucio
; APPLICANT: Robert I. Richards
; APPLICANT: Darrell O. Riecke
; APPLICANT: No. 6627745man A. Doggett
; APPLICANT: Moraechai Pras
; TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING
; TITLE OF INVENTION: FAMILIAL MEDITERRANEAN FEVER
; FILE REFERENCE: 14014.0314UI
; CURRENT APPLICATION NUMBER: US/09/486,147
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/US98/17255
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: 60/056,217
; PRIOR FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./ No. 6627745e =
; OTHER INFORMATION: Synthetic construct
US-09-486-147-36
Query Match 13.9%; Score 348; DB 4; Length 183;
Best Local Similarity 42.9%; Pred. No. 6.2e-25;
Matches 75; Conservative 28; Mismatches 68; Indels 4; Gaps 3;

QY 297 LTLDPGTAHORLLISDDCTTIVAYGNLHPQLQDSPKRFDVEVSVLGSEAFSSGVHYWEV 356
Db 3 MLLDPTSAHPNHLSDGLTSVRYGE-NKLSLPDNPKAFSCCIIVLGSGQFDSGRHYWEYE 61
QY 357 VAEKTQWVIGLAHEAASRKGSIQIOPSRGFYCIVMHDGNOYSACTEPWTRLNVRDKLV 416
Db 62 VGDKTAWDVGMASESSNRKGIKLNPKNGYWAIVLWNGNAYKALESPKSLSSHPRKI 121
QY 417 GYFLDYDQGLLIYFNADDMWLTREKPKGLCSYFSGQSHANGKNVQPLR 459
Db 122 GYVDYEGQISFYFNADDMWLTREKPKGLCSYFSGQSHANGKNVQPLR 173

RESULT 6
US-09-663-600A-198
; Sequence 198, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 198
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
US-09-663-600A-198
Query Match 14.6%; Score 364.5; DB 4; Length 413;
Best Local Similarity 26.4%; Pred. No. 6.2e-26;
Matches 115; Conservative 79; Mismatches 170; Indels 71; Gaps 15;
QY 4 SLKDELLCSICLSIQDPVSLGCHYFCRCRITETHWVQEA---QCARDCPCRRTFAE 59
Db 8 NVQSEVTCFICLELITELSLDCGHSICRACITVS--NKEAVTSMGGKSCPCVCGISYSP 65

Db 5 LDAETAYENLIPSDLLKVRIGNKW-ERLPDGPQRPDSCIIIVLGSPFSLSGRRYVEVVG 63
QY 359 EKTQWVIGLAHSAARSGSIQIQPSRGFGYCIYMHGNOYSACTEPWTRLNVRDKLDKGVG 418
Db 64 DKTAMILGACKTSISRKGNMTLSPENGYVVMIMKENEYQASSVPPTLLIKEPPKRVGI 123
QY 419 FLDYDQGLLIFYNADDMWMLYTFRE-KPFGKLCVSFSPQSHANGKNVOPRLI 470
Db 124 FVDYRVGSISFYVWTVARSHIYTFASCSFGPLQIPFSPG-TRDGGKNTAPLTI 175

RESULT 11

US-09-910-174B-18
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
Patent No. 6630575
GENERAL INFORMATION:
APPLICANT: Manning, Stephen
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174B
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 513
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-174B-18

QY 202 ADTARTLTDI-----EQKVORYSQQLRKVQEGAIQLQERLAETDRHTFLAGVA 249
Db 250 AALARTLPVLLLLGAGYFLWQQEKKYQPRKKRE--QELREMAWSTMKQEQSTRVK 307
QY 250 SLSE-----RLKGKIHTNLTYEDFTSKYTGLOQYTIW-KSLFQDIHPVPAALTD 300
Db 308 LLEELRWSRISQVASRGERSA-----YNEWKALFK-----PADVILD 345
QY 301 PGTAHORLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWEVVVAEK 360
Db 346 PKTANPILLVSEDQSRVQRAK-EPQDLDPNPERFNWHYCVLGCESTISGRHIWEVEVGDR 404
QY 361 TQWVIGLAHSAARSGSIQIQPSRGFGYCIYMHGNOYSACTEPWTRLNVRDKLDKGVGVL 420
Db 405 KEWHIGVCSKNVQKGVKMTPENGFWMTGLTDGNKYRTLTEPRTNLKLPKPKKVGVL 464
QY 421 DYDQGLLIFYNADDMWMLYTF 441
Db 465 DYETGDISFYNAVDSGHSHITF 485

RESULT 12

US-09-620-461-18
Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;
Patent No. 6630575
GENERAL INFORMATION:
APPLICANT: Manning, Stephen
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
FILE REFERENCE: 5800-149
CURRENT APPLICATION NUMBER: US/09/620,461
CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 513
TYPE: PRT
ORGANISM: Homo sapiens
US-09-620-461-18

Query Match 13.1%; Score 329; DB 4; Length 513;
Best Local Similarity 34.1%; Pred. No. 2e-22;
Matches 89; Conservative 40; Mismatches 86; Indels 46; Gaps 7;

QY 202 ADTARTLTDI-----EQKVORYSQQLRKVQEGAIQLQERLAETDRHTFLAGVA 249
Db 250 AALARTLPVLLLLGAGYFLWQQEKKYQPRKKRE--QELREMAWSTMKQEQSTRVK 307
QY 250 SLSE-----RLKGKIHTNLTYEDFTSKYTGLOQYTIW-KSLFQDIHPVPAALTD 300
Db 308 LLEELRWSRISQVASRGERSA-----YNEWKALFK-----PADVILD 345
QY 301 PGTAHORLILSDCTIVAYGNLHPQLQDSPKRFDEVSVLGSEAFSSGVHYWEVVVAEK 360
Db 346 PKTANPILLVSEDQSRVQRAK-EPQDLDPNPERFNWHYCVLGCESTISGRHIWEVEVGDR 404
QY 361 TQWVIGLAHSAARSGSIQIQPSRGFGYCIYMHGNOYSACTEPWTRLNVRDKLDKGVGVL 420
Db 405 KEWHIGVCSKNVQKGVKMTPENGFWMTGLTDGNKYRTLTEPRTNLKLPKPKKVGVL 464
QY 421 DYDQGLLIFYNADDMWMLYTF 441
Db 465 DYETGDISFYNAVDSGHSHITF 485

RESULT 13

US-08-724-394A-5
Sequence 5, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Rudy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:


```
/ LENGTH: 610 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..610
/ OTHER INFORMATION: /note= "BTF3"
US-08-724-394A-5

Query Match      12.6%; Score 321; DB 2; Length 610;
Best Local Similarity 34.7%; Pred. No. 1.5e-21;
Matches 82; Conservative 45; Mismatches 87; Indels 22; Gaps 8;

QY 218 YSQLRKVQGAQILQER-----LAETDRH-TFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLQYT 270
Db 287 WRQKEKIALSRETEREREMKEMGYAATEQESIXXXXXXKLEKLQELKWKRIQY---- 342
QY 271 TSKYTGPLQYTIWK-SLFQDIHPVPAALTLDPGTAHQRLILSDCTIYVAGNHLHQPQ--- 326
Db 343 MARGEKSLAYEWKALFK-----PADVILDPDTANAILLVSEDDQRSVQRAE-EPRDXXX 396
QY 327 LQSPKRFDEVSVLGSEAFSGVHYWEVVAETQWVIGLAHEAASR-KGSIQIQPSRG 385
Db 397 LPDNPPEFEMRYCVLGCENFTSGRHYWEVEGDKREWHIGVCSKNVERKKGWVKTPENG 456
QY 386 FYCIVMHDGNOYSACTEPWTRLNVRDKLDKVGVLFDYDQGLLIFYNADMSWLYTF 441
Db 457 YWTGLTDGNKYRALTEPTNLKLPFPPKRGIFLDYETGRISFYNATDGSHTYTF 512

RESULT 14
US-09-910-174B-10
; Sequence 10, Application US/09910174B
; Patent No. 6630575
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174B
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174B-10

Query Match      12.6%; Score 316.5; DB 4; Length 527;
Best Local Similarity 33.3%; Pred. No. 3.2e-21;
Matches 89; Conservative 38; Mismatches 93; Indels 47; Gaps 11;

QY 222 LRKVEGAQILQERLAETDRHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLQYT 281
Db 269 INKLQEKKKILSGE-KEFERETREIALKELEKERVQKEELQVKEK-----LQEE 317
QY 282 I-WKSLFQDIHPVPAALTLDPGTAHQRLILSD-----CTIVAYGNLHQPQLQDSPKRF 334
Db 318 LRMRRTF--LHADV--VVLDPDTAHPDLFLSEDRSRVRCRPFRLGSEVP-----DNPERF 369
QY 335 DVEVSVLGSFAFSGVHYWEVVAETQWVIGLAHEAASRKGSIQIQPSRGFYCIVMHDG 394
Db 370 DSQPCVLGRESFASGKHYYEVEVENVETVGVCRDSVERKGEVLLIPQNGFWLMEHKG 429
QY 395 NQYSACTEPWTRLNVRDKLDKVGVLFDYDQGLLIFYNADMSWLYT-----F 441
Db 430 -QYRAVSPDRILPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPQKLCVYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

Search completed: July 23, 2004, 15:09:01
Job time : 20 secs
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Db 430 -QYRAVSPDRILPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPQKLCVYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

RESULT 15
US-09-620-461-10
; Sequence 10, Application US/09620461
; Patent No. 6635750
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7
; FILE REFERENCE: 5800-149
; CURRENT APPLICATION NUMBER: US/09/620,461
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-461-10

Query Match      12.6%; Score 316.5; DB 4; Length 527;
Best Local Similarity 33.3%; Pred. No. 3.2e-21;
Matches 89; Conservative 38; Mismatches 93; Indels 47; Gaps 11;

QY 222 LRKVEGAQILQERLAETDRHTFLAGVASLSERLKGKHETNLTYEDPPTSKYTGPLQYT 281
Db 269 INKLQEKKKILSGE-KEFERETREIALKELEKERVQKEELQVKEK-----LQEE 317
QY 282 I-WKSLFQDIHPVPAALTLDPGTAHQRLILSD-----CTIVAYGNLHQPQLQDSPKRF 334
Db 318 LRMRRTF--LHADV--VVLDPDTAHPDLFLSEDRSRVRCRPFRLGSEVP-----DNPERF 369
QY 335 DVEVSVLGSFAFSGVHYWEVVAETQWVIGLAHEAASRKGSIQIQPSRGFYCIVMHDG 394
Db 370 DSQPCVLGRESFASGKHYYEVEVENVETVGVCRDSVERKGEVLLIPQNGFWLMEHKG 429
QY 395 NQYSACTEPWTRLNVRDKLDKVGVLFDYDQGLLIFYNADMSWLYT-----F 441
Db 430 -QYRAVSPDRILPLKESLCRVGVFLDYVEAGDVSYNNRDRSHIYTCPSAFSPVRPFF 488
QY 442 R---EKFPQKLCVYFSPQSHANGKV 465
Db 489 RLGCEDSPFIC-----PALTGANGVTV 511

Search completed: July 23, 2004, 15:09:01
Job time : 20 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 15:04:50 ; Search time 17 Seconds
(without alignments)
2687.704 Million cell updates/sec

Title: US-09-927-091-1
Perfect score: 2504
Sequence: 1 MACSLKDELLCSICLSIYQD.....GQSHANGKNVQLRINTVRI 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	31.1	624	S28418	probable zinc-bind
2	763.5	30.5	609	A43906	nuclear phosphopro
3	663.5	26.5	518	JC7387	testis-abundant fi
4	583	23.3	513	TVHURF	ret finger protein
5	572	22.8	506	S37583	RING finger protei
6	552.5	22.1	475	A37241	52K autoantigen Ro
7	472.5	18.9	477	JE0343	terf protein - rat
8	372.5	14.9	667	T09482	ring finger protei
9	370.5	14.8	438	T12494	hypothetical prote
10	364.5	14.6	667	T09013	RING finger protei
11	353.5	14.1	442	A57041	transcription regu
12	341	13.6	630	A49656	estrogen-responsiv
13	304.5	12.2	634	I49642	butyrophilin - bov
14	301.5	12.0	526	A37821	butyrophilin precu
15	293	11.7	526	S70587	regulatory protein
16	286.5	11.4	487	S65333	glioblastoma RING
17	276.5	11.0	365	A30891	hypothetical prote
18	259	10.3	551	JC7562	butyrophilin 1, B
19	258.5	10.3	801	TVHURE	butyrophilin 2, B
20	239.5	9.6	210	T46303	hypothetical prote
21	233	9.3	150	T28135	ring finger B-box
22	227	9.1	224	T28136	probable ataxia-te
23	224	8.9	792	T00082	hypothetical prote
24	213.5	8.5	638	JC7753	ring finger B-box
25	166.5	6.6	588	A49618	probable ataxia-te
26	161.5	6.4	331	T31998	hypothetical prote
27	161	6.4	698	T32840	hypothetical prote
28	158	6.3	375	T33778	hypothetical prote
29	158	6.3	375	F88947	protein C39F7.2 [i

30 155.5 6.2 574 2 S28275
31 155.5 6.2 974 2 E88549
32 145.5 5.8 412 2 D88072
33 145.5 5.8 808 2 T22363
34 142.5 5.7 675 2 T01112
35 140.5 5.6 1812 2 I49350
36 137.5 5.5 700 2 A61527
37 137 5.5 487 1 DBY18
38 133.5 5.3 560 2 A40044
39 133.5 5.3 589 2 A60198
40 133.5 5.3 589 2 S42517
41 133.5 5.3 589 2 S44381
42 133.5 5.3 593 2 B40045
43 133.5 5.3 633 2 S19244
44 133.5 5.3 641 2 A40045
45 133.5 5.3 802 2 S42518

RESULT 1
S28418
probable zinc-binding protein - Iberian ribbed newt
C:Species: Pleurodeles waltl (Iberian ribbed newt)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
C:Accession: S28418; S29476
R:Bellini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A:Title: A putative zinc-binding protein on lampbrush chromosome loops.
A:Reference number: S28418; MUID:93154311; PMID:7679068
A:Accession: S28418
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <BEL>
A:Cross-references: EMBL:L04190
R:Bellini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29476
A:Accession: S29476
A:Molecule type: mRNA
A:Residues: 1-263, 'LK', 266-624 <BE2>
A:Cross-references: EMBL:L04190; NID:g213867; PID:g213868
C:Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells an
C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:158-207/Domain: RING finger homology <RNG>

Query Match 31.1% Score 778; DB 2; Length 624;
Best Local Similarity 35.6%; Pred. No. 5e-41;
Matches 171; Conservative 81; Mismatches 193; Indels 36; Gaps 9;
QY 7 DELLCSICLSIYQDPVSLGCEHYFCRCITHEWVROAQAQARDCECRRTFAFPALAPSL 66
Db 158 EDLTCPLRSLRPEVILEGHNFCXCDKSM---ESASAFSCPECKEVLTERKYTNR 214
QY 67 KLANIVERTSYSPFDAILNARRARPCQAH-D-KVULFCLTDRALLCFDCEPALHEOHQV 125
Db 215 VLANLVKAAVGVKDKVFKP---EKCDHEHRLKLFCKDDGTACVICRDSKLHSHNF 271
QY 126 TGIDDAFDELQRELKDLQAL-----ODSERHEALQLLKRLAETFSSTKSL 174
Db 272 LPQDVG-----VYRQLIALVSPLETTKKNOKLKDQSQKTSLSHRENTVDCKKIEC- 326
QY 175 RTTIGFAFERLHRLRQKAMLELEADTARTLTIDIEQKVQVYSQQLRKVQGAQILOE 234
Db 327 -----EFEKLHQFLREKAKVVDLNAEGLLKQMEANLVKMTDNCFEIEAISTQS 380
QY 235 RLAEATRHRFLAGVASLSRL-----KGKIHETNLTYEDPPTSKYTPGLQYTIWKSIFQD 289
Db 381 RLNESDFIAFLTDIKSFIEKCEBHRKGVPAESVLNVKLSQGRFNPGLQYLIWKLKSV 440
QY 290 IHPVPAALTLDCTAHQRLJLSDDCITIVAGNLHLPQLQDSPKRFDVEVSLGSEAFSSG 349

Db 441 VQPGIAPLTLDPTAHNPLVLSGLTSVKYTDYTKQQLPDNPKRFSQICILVIGAEFGDSG 499
QY 350 VHYEVVVAETQWVIGLAHAASRKGSIQIOPGRGFCYIVMHDGNOYSACTEPTWRLNV 409
Db 500 KHYEVEVGNTADVGVNASSESRKKGKILNPKNGYWAIRNGNAFKALESFSLNL 559
QY 410 RDKLDKVGVDYFDQGLLIFYNADMSWLYTFREKPKGLCSYSPGSHANGKNVQPIR 469
Db 560 TSKEPSKIGVLDYEGQVSYFNADMSPLTYFNGSFTEKLYPYLSPFLQD-SGKNABPLK 618
QY 470 I 470
Db 619 L 619

RESULT 2
A43906
nuclear phosphoprotein xnf7 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: A43906; S27947
R:Reddy, B.A.; Kloc, M.; Etkin, L.
Dev. Biol. 148, 107-116, 1991
A:Title: The cloning and characterization of a maternally expressed novel zinc finger nu
A:Reference number: A43906; MUID:92038424; PMID:1936552
A:Accession: A43906
A:Molecule type: mRNA
A:Residues: 1-609 <RED>
A:CROSS-references: EMBL:M63705; NID:g214914; PID:g214915
A:Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBI:64520)
C:Genetics:
A:Gene: xnf7
C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:141-190/Domain: RING finger homology <RNG>

Query Match 30.5%; Score 763.5; DB 2; Length 609;
Best Local Similarity 35.4%; Pred. No. 3.9e-40;
Matches 167; Conservative 88; Mismatches 200; Indels 17; Gaps 9;
QY 7 DELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAGARDCEPCRRTFARPALAPSL 66
Db 141 BELTCLVELFDPVWVACGHNFPCSCIDKAW---EGQSFACPCRESITDRKTTINR 197
QY 67 KLANIVERYSSFPDLAINARRARPCQAHDKVKLFCLTDRLALLCFDDEPALHQBQHV 125
Db 198 VLANLAKKAACFTPTPEKKTREPLEKSEHDERLKYCKDDGTLSCVICHDSLKASHNF 257
QY 126 TGIDDAFDELQRELKQALQDSERHTEALQLLKRLAETKSTKSL---RTTIGFAF 182
Db 258 LPILDVAVGVVRELSAIVAPLEASLVK-TE--QLSSEQSDKIBQHNKNMSQYKEHITSEF 314
QY 183 ERHLRLRERQKAMLEBEADTARTLTDIEQVORYSQQLRQVQGAQILQERLAETDRH 242
Db 315 EKLHFLREERKLELQKEGNNLTPEMNNLVKQESQDAIKKILSIKAKERMEDTDSI 374
QY 243 TEL---AGVASISERLKGKHETN-LTYEDFPTSKYTGFLQYTIWKSFLQDTHPVPAL 297
Db 375 SFLMDIKAFIDKCEQRAVISTGNLTLSKELCGTFKPIQYIMWKEKSVVIPSITPM 434
QY 298 TLDPGTAHORLILSDDCITVAYGNLHPQLODQSPKRDVEVSLGSEAPSGVHYWVWV 357
Db 435 LLDPTSAPNHLHSLDGLTSVRYGE-NKLSLDPNPKRFSQICILVIGAEFGDSG 493
QY 358 AETQWVIGLAHAASRKGSIQIOPGRGFCYIVMHDGNOYSACTEPTWRLNVRDKLVG 417
Db 494 GDKTAMDVGWASSSESRKKGKILNPKNGYWAIRNGNAFKALESFSLSHPRKIG 553
QY 418 VFLLDYDQGLLIFYNADMSWLYTFREKPKGLCSYSPGSHANGKNVQPIR 469
Db 554 VYVDYEGQISFYFNADMSWLYTFNATTEKLYPYLSP-FLHDSGKNVDPLR 604

RESULT 3
JC7387
testis-abundant finger protein - human
C:Species: Homo sapiens (man)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7387
R:Orimo, A.; Yamagishi, T.; Tominaga, N.; Yamauchi, Y.; Hishinuma, T.; Okada, K.; Suzuki
Biochem. Biophys. Res. Commun. 276, 45-51, 2000
A:Title: Molecular cloning of testis-abundant finger protein/ring finger protein 23 (RNF
A:Reference number: JC7387
A:Contents: Testis
A:Accession: JC7387
A:Molecule type: mRNA
A:Residues: 1-518 <ORI>
A:CROSS-references: DBJ:AB046381
C:Comment: This protein, a member of the ring-B box-coiled coil-B30.2 protein family, p1
C:Genetics:
A:Gene: tfp
A:Map position: 6p21.3-6p22.1
A:Introns: 151/3; 183/3; 260/3; 268/2; 298/2; 337/1
C:Superfamily: rfp transforming protein; RING finger homology
C:Keywords: coiled coil; testis
Query Match 26.5%; Score 663.5; DB 2; Length 518;
Best Local Similarity 32.8%; Pred. No. 5.5e-34;
Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;
QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAGARD--CPECRTFAEPA 61
Db 22 NLQVEASCSVCLEYLKEPVIECGHNFCKACITRWEDLE---RDFPCVCRKTSRYRS 77
QY 62 LAPSILKLANIVERYSSFPDLAINARRARPCQAHDKVKLFCLTDRLALLCFDDEPALH 120
Db 78 LRPNQLGSWVE--IAKQLQAVRKIRDESCLPCQHEALSLFCYEQEAVCLICATSHTH 135
QY 121 EHQVTVGIDDAFDELQRELKQALQDSERHTEALQLLKRLAETKSTKSLRTTIGE 180
Db 136 RHTVTVPLDDATQCYEKEKLEKQLEPLEQKLEITRCKSSEKKPGELKELVESRQILR 195
QY 181 APERLHLRLRERQKAMLEBEADTARTLTDIEQVORYSQQL-----RK 224
Db 196 EPEELHRLDEEQVLLSRLEEE---QDILQLRENAHAHGDGDKRRDLAHLAEVEGKC 251
QY 225 VQEGAQILQERLAETDRH---TFLAGVASLSER---LKGKIHETNLTYEDFPTSKYTG- 276
Db 252 LOSGFEMLKDVKSTLEKNIIPRFGGSLTICPRDHKALLGLVKEIN-RCEKVKTMETSV 310
QY 277 -----PLQY-----TIWKSFLQDTHPVPALTLDPGTAHORLILSDDCITVAYGN 321
Db 311 SIELEKNFSNFPQYFALRKILKQLIADV-----TLDPETAHPNLVLSEDRSKVFVE 363
QY 322 LHPQLODQSPKRDVEVSLGSEAPSGVHYWVWVVAETQWVIGLAHAASRKGSIQIQ 381
Db 364 TLRLDLPDTPRRFTFYPCVLATEGFTSGRHYWEVGDGKTHWAVGCRDVSARKGETPL 423
QY 382 PSRGFCYIVMHDGNOYSACTEPTWRLNVRDKLVGVDYDQGLLIFYNADMSWLYTF 441
Db 424 PETGVKRVRLWNGDKVAATITPTPLHLKVPKRVGLFIDYEAGTLSFYNVNDRSHIYTF 483
QY 442 REKFPFGKLCYSFGSGSHANGKNVQPIRI 470
Db 484 TDIPTFTEKLWPLFVPG-IRAGKNAAPLTI 511
RESULT 4
TVHURF
ret finger protein - human
N:Alternate names: transforming protein rfp
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jan-2001
C:Accession: A28101
R:Takahashi, M.; Inaguma, Y.; Hiai, H.; Hirose, F.

Mol. Cell. Biol. 8, 1853-1856, 1988
A;Title: Developmentally regulated expression of a human "finger"-containing gene encode
A;Reference number: A28101; MUID:88246464; PMID:3380101
A;Accession: A28101

A;Molecule type: mRNA

A;Residues: 1-513 <TAK>

A;Cross-references: DDBJ:J03407; NID:g337371; PIDN:AAA36564.1; PID:g337372

C;Genetics:

A;Gene: GDB:RFP

A;Cross-references: GDB:511359; GDB:1391662

A;Map position: 6p22-6p21.3

C;Superfamily: rfp transforming protein; RING finger homology

C;Keywords: DNA binding; transforming protein; zinc finger

F;1-315/Product: transforming protein rfp (fragment) #status predicted <RET>

F;12-62/Domain: RING finger homology <RNG>

F;16-127/Domain: metal and nucleic acid binding #status predicted <TMN>

F;16-56/Region: zinc finger C3HC4 motif

Query Match 23.3%; Score 583; DB 1; Length 513;
Best Local Similarity 29.1%; Pred. No. 5.7e-29;
Matches 153; Conservative 89; Mismatches 178; Indels 106; Gaps 16;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITEHVWVROEAQAGARDPCPCRTFAEPALAP 64

Db 10 LQQTTCPCVCLQYFAEPWMLDCHNICCAACARCGTAEATNVS--CPQRETFPQHRMP 67

QY 65 SLKLANIVERYSSPFLDALNARRARP-----COAH-DKVKLFLCTDRALLCFPC 114

Db 68 NRHLANTQ-----LVQLTERPSGGMGVCEKREPLKLYCEEDQMPICVVC 118

QY 115 DEPALHEQHVGTGIDDAFDELQRELKQALQADSEREHTALQLLRQ-----LAE 166

Db 119 DRSREHRGHSVLPLEAVEGFEKQIQNL-----DHLKRVKDKKRRRAQGEQARAE 170

QY 167 TKSSTKSRTTIGAFERLHLRLB---RQKAMLELE-----ADTA 205

Db 171 LLSLTOMERKIVWEFEQYHSLKEHEVRLARLELDLAITYNSINGAITQFSCNISHLS 230

QY 206 RLTLDIEQKVORYSQOLRKVQGAQILQERLAETDR-----HTFLAGV 248

Db 231 SLIAQLBEKQOQPTREL-----IQDLDGTLRSRAERIRPEPWITPPDLOEKIHFAKQC 284

QY 249 ASLSERLKGKHETNLTYEDPFTSGTPQYTIWKSIFQDIHPV---PAALTLDPGTAH 305

Db 285 LFLTESLK-----QFTEKQSDMEK--IQELREAQLYSDVTLDPDTAY 326

QY 306 QRLTSDCTIVAYGNLHPQLODPSKRFVSVVLGSEAFSSGVHVVVAEKTQWVI 365

Db 327 PSLTSLNLRQVRSYLIQ-QDLPNPERFNLFPCLVGLSPCFIAGRHYWEVEVGDKAKWTI 385

QY 366 GLAHEAASRKGSIQIQPSRGFYCIWHDGNQYSACTEPWTLNRVDRKLDKGVFLDYDQ 425

Db 386 GVCEDSVCRKGGVTSAPQNGFWAIVSLWYKEYWALTSPMTALPLRTPLQRVGIFLDYDAG 445

QY 426 LLIFYNADMSWLYTF-REKFPKGLCSYFSPGQSHANGKNVQPLRI 470

Db 446 EVSFYNVTERCHTFTSHATFCGPVPYFS--LSYSGKSAAPLI 489

RESULT 5

S37583

RING finger protein rfp - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999

C;Accession: S37583

R;Takahashi, M.

Submitted to the EMBL Data Library, October 1993

A;Reference number: S37583

A;Accession: S37583

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-506 <TAK>

A;Cross-references: EMBL:X75343; NID:g406747; PIDN:CAA53092.1; PID:g406748

C;Superfamily: rfp transforming protein; RING finger homology

C;Keywords: zinc

F;5-55/Domain: RING finger homology <RNG>

Query Match 22.8%; Score 572; DB 2; Length 506;

Best Local Similarity 28.5%; Pred. No. 2.7e-28;

Matches 148; Conservative 88; Mismatches 190; Indels 94; Gaps 14;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITEHVWVROEAQAGARDPCPCRTFAEPALAP 64

Db 3 LQQTTCPCVCLQYFVPEWMLDCHNICCAACARCGTAEATNVS--CPQRETFPQHRMP 60

QY 65 SLKLANIVERYSSPFLDALNARRARP-----COAH-DKVKLFLCTDRALLCFPC 114

Db 61 NRHLANTQ-----LVQLTERPSGGMGVCEKREPLKLYCEEDQMPICVVC 111

QY 115 DEPALHEQHVGTGIDDAFDELQRELKQALQADSEREHTALQLLRQ-----LAE 166

Db 112 EPSREHRGHSVLPLEAVEGFEKQIQNL-----DHLRVRKDKKRRRAQGEQARAE 163

QY 167 TKSSTKSRTTIGAFERLHLRLB---RQKAMLELEADTARTITDIEQKVORYS----- 219

Db 164 LLSLTOMERKIVWEFEQYHSLKEHEVRLARLELDLAITYNSINGAITQFSCNISHLS 223

QY 220 -----QQLRKVQGAQILQERLAETDR-----HTFLAGVASLSER 254

Db 224 GLIAQLBEKQOQPTRELQDGLTSLRAERIRPEPWITPPDLOEKIHFAKCLFLTES 283

QY 255 LKGIKHETNLTYEDPFTSGTPQYTIWKSIFQDIHPV---PAALTLDPGTAHQLRLS 311

Db 284 LK-----QFTEKQSDMEK--IQELREAQLYSDVTLDPDTAYPSLLS 325

QY 312 DDCTIVAYGNLHPQLODPSKRFVSVVLGSEAFSSGVHVVVAEKTQWVIGLAHEA 371

Db 326 DNLQVRSYLIQ-QDLPNPERFNLFPCLVGLSPCFMAGRHYWEVEVGDKAKWTIGVCEDS 384

QY 372 ASRKGSIQIQPSRGFYCIWHDGNQYSACTEPWTLNRVDRKLDKGVFLDYDQGLLIFYN 431

Db 385 VCRKGGVTSAPQNGFWAIVSLWYKEYWALTSPMTALPLRTPLQRVGIFLDYDAGEVSFN 444

QY 432 ADDMSWLYTF-REKFPKGLCSYFSPGQSHANGKNVQPLRI 470

Db 445 VTERCHTFTSHATFCGPVPYFS--LSYSGKSAAPLI 482

RESULT 6

A37241

52K autoantigen Ro/SS-A - human

N;Alternate names: Sjogren syndrome antigen A

C;Species: Homo sapiens (man)

C;Date: 07-Feb-1992 #sequence_revision 26-May-1995 #text_change 17-Mar-2000

C;Accession: A55642; A37241; A37240

R;Tsugu, H.; Horowitz, R.; Gibson, N.; Frank, M.B.

Genomics 24, 541-548, 1994

A;Title: The location of a disease-associated polymorphism and genomic structure of the

A;Reference number: A55642; MUID:95229155; PMID:7713506

A;Accession: A55642

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-475 <TSU>

A;Cross-references: GB:U13657

R;Itoh, K.; Itoh, Y.; Frank, M.B.

J. Clin. Invest. 87, 177-186, 1991

A;Title: Protein heterogeneity in the human Ro/SSA ribonucleoproteins. The 52- and 60-kD

A;Reference number: A37241; MUID:91086445; PMID:1985094

A;Accession: A37241

A;Molecule type: mRNA

A;Residues: 1-475 <TAK>

A;Cross-references: GB:M34551; NID:g337484; PIDN:AAA36581.1; PID:g337485

R;Chan, E.K.L.; Hamel, J.C.; Buyon, J.P.; Tan, E.M.

J. Clin. Invest. 87, 68-76, 1991

A;Title: Molecular definition and sequence motifs of the 52-kD component of human SS-A/Ro

A;Reference number: A37240; MUID:91086480; PMID:1985112

Db	6	LARRLOBEATCSICLDYFDTPVMTAGHNFCECIQMSWEKGKXGKKQKQSGFPCPEC	65
Qy	54	RTTFAPALAPSILKLANIVERYSSFLDALINARRAARPCQAH-DKVKLFCLTDRLALLCF	112
Db	66	REMSPOBNLPNLLTKVAEMARQHP---GLHKRDL---CQIHQEPKLKFCQDDQTPICV	119
Qy	113	FCDEPALHGOHVGTGIDDAFDEIQRELUQLOALQDSEREHTTALQLLKQ-LAETXSST	171
Db	120	VCREAQEHRRHVRVLPDEAAREYKLEEDIKYIRE-EMMKTTLOAKESQTLTEWQERV	178
Qy	172	KSRLTTIGEAFAERLHLLREROKAMLEEL---EADTARTLTDTEQVQRYSQOLRKV---	225
Db	179	KERRERLLEEFQKVVLFLVEEERPLLOILKKEEDDTLCKLODSKASLDHQSRSLDILLQ	238
Qy	226	-----QEGAOIILQERLAETDRHTFLAGVASLSERLKGKIHETNLTVEDEPTSKYT---G	276
Db	239	LEEQTOQEPLQMLQD-----VKDITLTKRESLSMQYPEVVL-----PVAIKTVCRV	283
Qy	277	PLQVTTWKSFLQDHPHPAALTDPGTAHQRLILSDDCITVAVGN-----LHPQLOQSP	331
Db	284	PGQIEVLKSFQEDVVP-----DPSATPYLLL-----YESQRRVLSPPPEGAP	328
Qy	332	---KRPQVEVSVLGSEAFSSGWHWEV---VVAETQWVIGLAHPAASRKSIOIQPREGF	386
Db	329	YSKDRFLAYPCAVGQKQSFSSGRHYWEGMMLTGDALWALGVCRDNVSEKRVLXSPENG	388
Qy	387	YCIVMHDGNOYSACTEPWTIRLVNRDKLDKGVPLDYDQGLILI FYNADDMSLMYTFRE-KF	445
Db	389	WVWQLSGKXGKHLPLLPNSIPVTLTEPSHMGIFLDFQAGEVSFYVNDGSHLHFSQVAF	448
Qy	446	PGKLCSYFSPGQSHANGKNVQPIRINTV	473
Db	449	PGPULLPFFCLG-SPKSGQMV-----ISTV	471

RESULT 8
T09482
ring finger protein FXY - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human FXY maps to chromosome Xp22.3: Implications for evolution
A:Reference number: Z16687
A:Accession: T09482
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: EMBL:AF035360; NID:g2827993; PID:g2827994
C:Genetics:
A:Gene: FXY
A:Map position: Xp22.3
C:Superfamily: RING finger homology
F:6-65/Domain: RING finger homology <RBN>

[illegible]

A:Accession: A37240
A:Molecule type: mRNA
A:Residues: 1-51, A_53-475 <CH>
A:Cross-references: GB:M62800; NID:g338489; PIDN:AAA36651.1; PID:g338490; GB:M35041
C:Genetics:
A:Gene: GDB:SSA1
A:Cross-references: GDB:I33758; OMIM:109092
A:Map position: 11p15.5-11p15.5
A:Introns: 136/3; 168/3; 245/3; 253/2; 287/1
C:Superfamily: rfp transforming protein; RING finger homology
C:Keywords: DNA binding; nucleus; zinc finger
F:12-60/Domain: RING finger homology <RNG>
F:16-54/Region: zinc finger C3HC4 motif

	Query Match	22.1%;	Score 552.5;	DB 1;	Length 475;
	Best Local Similarity	31.3%;	Pred. No. 4.1e-27;		
	Matches 150;	Conservative 88;	Mismatches 208;	Indels 33;	Gaps 14;

Qy	7	DELCSICLSIVDYDPVSLGCEHYFCRCITHEWVROEAQACRCPCEGRTFAEPALAPSL	66
Db	12	EEVTCPICLDPFVEPVSIECGHSFQECISQ-----VKGGGGVCPVCQRQLLNLRNPR	67
Qy	67	KLAMIVERYSPFLDAILNARRAARPCQAH-DKVKLFCLTDRALLCFPCDEPALHEQHV	125
Db	68	QLANVNVLKELISQEA--REGTQGERCAVHGERLHLFCXDKGKALCWCAQRKXRDHAM	125
Qy	126	TGIDDAFDELQELKDQLQALQDSREHTEALQI----LKQLAETKSTSKSLRTTIGFAF	182
Db	126	VPLEEAAQEQYQELQVALGELR-RKQELAEKLEVEITAIRK--ADWKKTVEQKRIHAEF	182
Qy	183	ERLHLLRERQKAMLEELLEADTARTITDTEQKVQVSQQLRKVKQEGAIQLQERLAETDRH	242
Db	183	VQQKNFLVEEQRQCELEKDEFEQLRIILGEKAQAQ-----SQALQELISELDRR	235

	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db
236	CHSSALELLQEVII	VILRGESNNLKDD	DIITSPELRSVCHV	PGLKKMLRTCAVH	-----IT	290			
299	LDPGTAHQRLIIS	DDCTIYAYGNLHP	QPLQDSPKRFDEVS	VLGSEAFSSGVHY	VEVVVA	358			
291	LDPDTANPWLII	LSSEDRRQVRLG	DTQ-QSI	PGNEERFDSY	PMVLGAQHFS	GKHYYEVDVT	349		
339	EKTQWVIGLAHEA	ASKGSITQIPSRG	FYCIQPSVHMDG	NGQYSACTBP	WTSLNVRD	KLDKGVV	418		
350	GKEANDLGVCRS	VRRRGHFLLSK	SGFWIWLWNKQ	KYECITYPTQ	PLHLQVPC	QVGI	409		
419	FLDYDQGLLI	FYN-ADDMGLY	TFRE-KFPGK	LCSYFSPGQ	SHANGKXV	QPLRINTVRI	475		
410	FLDYEAGMVSY	FNITDGHSLIY	SFSECAFTG	PLRFFSPG-F	NDGGKN	TAPLTLQPLNI	467		

RESULT 7
JE0343
terf protein - rat
;Species: Rattus norvegicus (Norway rat)
Tel:1999 #test charz 09-Jun-2000

C/Accession: JEO343
R/Ogawa, S.; Goto, W.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramatsu, M.; Inoue, S.
Biochem. Biophys. Res. Commun. 251, 515-519, 1998
A>Title: Molecular cloning of a novel RING finger-B box-coiled coil (RBCC) protein, termed
A/Reference number: JEO343; MUID:99011410; PMID:9792805
A/Accession: JEO343
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-477 <OGA>
C/Superfamily: rfp transforming protein; RING finger homology
F,12-71/Domain: RING finger homology <RRN>

Query Match 18.9% Score 472.5; DB 2; Length 477;
Best Local Similarity 28.9%; Pred No. 4e-22;
Matches 147; Conservative 81; Mismatches 203; Indels 77; Gaps 19;

```
QY 99 VKLFCLTDRLALCFCCDEPALHEQHCVTGIDDAFDELORELKQLOAL--QDSEREHTEA 156
Db 183 VNMVCTDDQLICALCKLVGRHRDQVAALSERYDKLQNLNLTNLKRNTELETLIA 242
QY 157 LQLLKRQLAETKSSKSLRTTIGEAFLRLRLRRERQKAMLEELADTARTLTIDIEQKVQ 216
Db 243 KLIQTCQHVENVASRQEAALT--EBCDLLIEIIQORRQIIGTKIKEGKVMRLKLAQQA 300
QY 217 RYSQQLRKVOEGAQILQERLAETDRHTFLAGVASLSERL-----KGKIHTNL--TYE 267
Db 301 NCKQCIERSASLISOAHSKENDHARFLQTAKNITERVSMATASSQVLIPEINLNDTFD 360
QY 268 ----DFPTSK-----YTGP-----KSLFQDIHPVPA-- 420
Db 361 TFALDFSREKKLLECLDYLTAHPNPPIREELCTASYDTITVHWTSDDEFSVSYELQYTI 420
QY 283 ----W-----KSLFQDIHPVPA-- 296
Db 421 FTGQANVSVLCSNADSMWIVPNIKQNHVTVHGLQSGTKYIFMWKAINQAGRSSEPGKIK 480
QY 297 ----LTLDPGTAHORLILSDDCITIVAGNLHPQPLQDS-----PKFDFEVS--VLGS 343
Db 481 TNSQPFKLDPKSARKLKVSHD-----NLTVDERDESSKKSHPTPERFTSQSGYGVAGN 533
QY 344 EAFSSGVHYWEVVAEKTQWVIGLAHEAASRKSGSIQIQRSGFYC-----IVMHDGNQY 397
Db 534 VFIDSGRHYWEVVTGSTWYALGLAYRSAPKHEWIGKNAASWALCRCHNHVAVRHDKGK 593
QY 398 SACTEPWTRLNVKRLDKGVFLDYDQGLLIFYNADMSWLYTFREKFPGLKCSYFS 454
Db 594 PIEPAPHLR-----RVGILLDYNGSIAFYDALNSIHLTYFDVAFAPQVPCVTF 642

RESULT 9
Tl2494
hypoetical protein DKFZp434C091.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Sep-1999
C:Accession: Tl2494
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17525
A:Accession: Tl2494
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <POU>
A:Cross-references: EMBL:AL080170
A:Experimental source: adult testis; clone DKFZp434C091
C:Genetics:
C:Note: DKFZp434C091.1
C:Superfamily: rfp transforming protein; RING finger homology

Query Match 14.8%; Score 370.5; DB 2; Length 438;
Best Local Similarity 30.2%; Pred. No. 8.3e-16;
Matches 105; Conservative 56; Mismatches 140; Indels 47; Gaps 9;

QY 126 TGIDDAFDELORELKQLOALQDSERHTEALQLLKROL--ARTKSTKSLRTTIGE--- 180
Db 80 SGALGAADWLAVQVKLQ-----ALELMKELEDAITQANVGKTVIWKVKV 127
QY 181 -----AFERHLRLRRERQKAMLEELPADTARTLTIDIEQVQRYSQQLRKVQEGAQI 231
Db 128 EMQORFRLEFEXHGFQLAQEQRLRLAEERATLQRLRESKSLVQOSKALKELADE 187
QY 232 LQERLAETDRHTFLAGVASLSERLKGKIHTNLTYEDFPFTSKYTG---PLOYTINWLSLFQ 288
Db 188 LQER-CORPALGULEGVRGVLSSKA---VTRLEAENIPMELKTACICPGRELLRKFQV 243
QY 289 DIHPVPAALTLDPGTAHORLILSDDCITIVAGNLHPQPLQD---SPKRFDEVSVLGSEA 345
Db 244 DV-----KLDPATAPSLLLTADLRSVDG-----EPWMDVNNPNERFDTPWPCILGLQS 292
QY 346 FSSGVHYWEVVAEKTQWVIGLAHEAASRKSGSIQIQRSGFYCIVMHDGNQYSACTEPWT 405
```

```
Db 293 FSSGRHYEVLVGEAEFWGLGVCQDTLPRKGTMPSPENGWALMLLKGYMWLASPSV 352
QY 406 RLNVARDKLDKGVFLDYDQGLLIFYNADMSWLYTFREKFPGLKCSYF 453
Db 353 PLLQLESFRCIGFLDYEAEGISFNVVDGSIYTFNQLFSGLLRPYF 400

RESULT 10
RING finger protein Fxy - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Sep-2000
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A:Title: A gene spans the pseudautosomal boundary in mice.
A:Reference number: Z16531; MUID:98004518; PMID:9342357
A:Accession: T09013
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PAL>
A:Cross-references: EMBL:AF026565; NID:g2589222; PIDN:AAB81986.1; PID:g2589223
C:Genetics:
A:Gene: Fxy
A:Map position: X; Y
C:Superfamily: RING finger homology
C:Keywords: zinc finger
F:6-65/Domain: RING finger homology <RNN>

Query Match 14.6%; Score 364.5; DB 2; Length 667;
Best Local Similarity 21.8%; Pred. No. 3.4e-15;
Matches 143; Conservative 87; Mismatches 204; Indels 223; Gaps 23;

QY 4 SLKDELLCSICLSIYQDPVSLGCEHYFCRR-----ITEHWVRQ---BAQAGDCPECRR- 55
Db 3 TLESELTCPICLELFEDPLLPCHSLCFNCAHRLVSHCATNEPVPESINAFQCTCRHV 62
QY 56 -TFAB---PALAPSLKLANIVERYS-----SPLDAILNAR----- 87
Db 63 ITLSQRLGDLGRNVTLQNIIDRFQKASVSGPNSPSTRERRAFDANTMSAEKVLQCF 122
QY 88 -----RAARP-----COAH--DK 98
Db 123 DQPAQDAVKTCVTCEVSYCDECLKATHPNKPFPTGHRLEIPDPSHIRGLTCLHEDEK 182
QY 99 VKLFCLTDRLALCFCCDEPALHEQHCVTGIDDAFDELORELKQLOAL--QDSEREHTEA 156
Db 183 VNMVCTDDQLICALCKLVGRHRDQVAALSERYDKLQNLNLTNLKRNTELETLIA 242
QY 157 LQLLKRQLAETKSSKSLRTTIGEAFLRLRLRRERQKAMLEELADTARTLTIDIEQKVQ 216
Db 243 KLIQTCQHVENVASRQEAALT--EBCDLLIEIIQORRQIIGTKIKEGKVIKRLKLAQQA 300
QY 217 RYSQQLRKVOEGAQILQERLAETDRHTFLAGVASLSERL-----KGKIHTNL--TYE 267
Db 301 NCKQCIERSASLISOAHSKENDHARFLQTAKNITERVSMATASSQVLIPEINLNDTFD 360
QY 268 ----DFPTSK-----YTGP-----KSLFQDIHPVPA-- 420
Db 361 TFALDFSREKKLLECLDYLTAHPNPPIREELCTASYDTITVHWTSEDFSVSYELQYTI 420
QY 283 ----W-----KSLFQDIHPVPA-- 296
Db 421 FTGQANVSVLCSNADSMWIVPNIKQNHVTVHGLQSGTKYIFTVKAINQAGRSSEPGKIK 480
QY 297 ----LTLDPGTAHORLILSDDCITIVAGNLHPQPLQDS-----PKFDFEVS--VLGS 343
Db 481 TNSQPFKLDPKSARKLKVSHD-----NLTVDERDESSKKSHAPERFAGQSGYGVAGN 533
QY 344 EAFSSGVHYWEVVAEKTQWVIGLAHEAASRKSGSIQIQRSGFYC-----IVMHDGNQY 397
Db 534 VFIDSGRHYWEVVTGSTWYALGLAYRSAPKHEWIGKNAASWALCRCHNHVAVRHDKGK 593
```

QY 398 SACTEPWTRNVRDKLKVGVFLDYDQGLLIPYNADMSWLYTTRKPPGKLCVSFS 454
 Db 594 PIAPAPHLR-----RVGVLLDYDNGSIAPYDTLSSVHLHTTHAALQAPVCPTFT 642

RESULT 11
 A57041
 transcription regulator Staf-50 - human
 N:Alternate names: stimulated trans-acting factor of 50K
 C:Species: Homo sapiens (man)
 C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 24-Sep-1999
 C:Accession: A57041
 R:Tissot, C.; Mechti, N.
 J. Biol. Chem. 270, 14891-14898, 1995
 A:Title: Molecular cloning of a new interferon-induced factor that represses human immunodeficiency virus type 1 transcription
 A:Reference number: A57041; MUID:95318041; PMID:7797467
 A:Accession: A57041
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-442 <RES>
 A:Cross-references: EMBL:X82200; NID:g899299; PIDN:CAA57684.1; PID:g899300
 C:Genetics:
 A:Gene: GDB:STAF50
 A:Cross-references: GDB:605574
 C:Superfamily: mouse regulatory protein rpt-1; RING finger homology
 C:Keywords: nucleus; zinc finger
 F:11-65/Domain: RING finger homology <RNG>

Query Match 14.1%; Score 353.5; DB 2; Length 442;
 Best Local Similarity 25.4%; Pred. No. 9.7e-15;
 Matches 112; Conservative 78; Mismatches 172; Indels 79; Gaps 15;

QY 5 LKDELCSICLSIYQDPVSLGCEHYFCRRCTIETHWVROE---AQGARDCEPCRRTPAEP 61
 Db 9 IKEVTCPCLELLEPLSLDCHGSCQACITAK-IKESVIISRGSSCEPVCQTRFQPGN 67
 QY 62 LAPSILKLANIVERYSPFDLAINARRAPCOAH-DKVKFLCLTDRLALCFPCDEPALH 120
 Db 68 LRPNRHLANIVERVKVMSPQSGQRDV--CBHGGKGLQIFCKDGKVICWVCELSQEH 125
 QY 121 EQHVTGIDDAFDELQELKDQAL--QDSREHTEALQLKRLAETKSKTSKSLRTTI 178
 Db 126 QGHOTFRINEVKECEKQLQVALRLIKEDQAEK-----LEDDIRQETAWKIERQKI 179
 QY 179 GEAFERLHLRLRRQKAMLEELADTARTLTDIEQVORYSQQLRVKQVQGAQLQERLA- 237
 Db 180 LKGFENMRVLDNEEQRELQKLEEGEVNLDNLAATAADQLVQKQDASTLISDLQRLTG 239
 QY 238 -----ETDRHTFLAGVASLSERLKGKIHETNLTIEDFTSKYTGPIQYTIWK 284
 Db 240 SSVEMQLQDVDMKRSESWTLKKPKSVSKLKSFRVFDL-----SGMLQ--VLK 287
 QY 285 SLFDQIHVPFAALTDPGTAHQRLILSD-----CTIVAYGNLHPQLQDSPKRF 335
 Db 288 EL-TDQYVWDVNLNPGSATNSVAISVDQKVTETCI--FKNSNPCDFG----- 336
 QY 336 VEVSVLGSEAFSGSVHYWEVVAETQWITGLAHAAS-----RKGS-----I 378
 Db 337 -AFGVFGQYFSSGKYWEVDVSKIAWILGVHSHKISSLNKRKSSGFAFDPSVNYSKVYS 395
 QY 379 QIOPSRGFYCIWHDGNOYSA 399
 Db 396 RYRPQYGVWIGLQNTCEYNA 416

RESULT 12
 A49656
 estrogen-responsive finger protein, efp (RING finger, coiled-coil domains) - human
 C:Species: Homo sapiens (man)
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A49656
 R:Inoue, S.; Orlimo, A.; Hosoi, T.; Kondo, S.; Toyoshima, H.; Kondo, T.; Ikegami, A.; Oud

Proc. Natl. Acad. Sci. U.S.A. 90, 11117-11121, 1993
 A:Title: Genomic binding-site cloning reveals an estrogen-responsive gene that encodes a transcription factor that represses human immunodeficiency virus type 1 transcription
 A:Reference number: A49656; MUID:94068555; PMID:8248217
 A:Accession: A49656
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-630 <INO>
 A:Cross-references: GB:D21205; NID:g458725; PIDN:BAA04747.1; PID:g458726
 A:Experimental source: placenta
 A>Note: sequence extracted from NCBI backbone (NCBIN:140455, NCBIP:140456)
 C:Superfamily: RING finger homology
 C:Keywords: zinc
 F:9-59/Domain: RING finger homology <RNG>

Query Match 13.6%; Score 341; DB 2; Length 630;
 Best Local Similarity 21.7%; Pred. No. 9.2e-14;
 Matches 139; Conservative 87; Mismatches 195; Indels 220; Gaps 25;

QY 3 CSLKDELCSICLSIYQDPVSLGCEHYFCRRCTIETHWVROEAGQARD-CPBCRRTF-APP 60
 Db 5 CPLAEELSCSICLEPFKEPVTTPCGHNTFCGSLNETWA---VQGSPLYLCPQCRVYQARP 61
 QY 61 ALAPSLKLANIVERYSSP-----PLDALLNARRARP----- 92
 Db 62 QLHKNTVLNVEQFLQADLAREPPADVWTPPARASAPSPNAQVACDCHLKEAAVKTCLV 121
 QY 93 -----COAH-----DKVKFLCLTDRLALCFPCDEPA----- 118
 Db 122 CWASFCQELHLPDFSPAPQDHPLOPPVVDLLRRKCSQHNRLREFPCPEHSECHICLIV 181
 QY 119 LHEQHVTGIDDAFDELQELKDQALQDSREHTEALQLKRLAETKSKTSKSLRTTI 178
 Db 182 EHKTCSPASLSQASADLEATLRHKLTVMSQ-----INGASRALDDVNRQDDVRMTA 234
 QY 179 GEAFERLHLRLRRQKAMLEELADTARTLTDIEQVQVOR-----YSQQLRVKQVQGAQLIQ 233
 Db 235 NRKVEOLOQOYEYTE-MKALLDASETTSTRKIKKEEKRVNSKFDITVQILKKSE-IQTLK 292
 QY 234 ERLAE--TDHHTF-----LAGVAS-----LSERLKGKIHETNL----- 264
 Db 293 EEIEQSLTRDDEFEFLKASKLKGISTKPVYIPEVELNHKLKGIHQSTIDLKNEKQCI 352
 QY 265 -----TVEDFTSKYTGPIQYTIWKSIFQDIH-----PVPA----- 295
 Db 353 GRLEUPTSSGDGDEHPASTHKSTRPV-----KTVSKEEKKSKPPVPALPSKLTFTG 407
 QY 296 -----ALTLDPGTAH 305
 Db 408 APEQLVDLQKAGLEAAKATSSHPNSTSLKAKVLETFLAKSRPELLEYIKVILDYNTAH 467
 QY 306 QRLILSDGCTIVAYGNLHPQLQDSPKRFDEVSIVLGSEAFSGSVHYWEVVAETQWIT 365
 Db 468 NKVALSECYTVASVAEM-PQNYRPHQRFYTCQVGLGHCHYKKGKGIHYWEVELQKNFPGV 526
 QY 366 GLAHEAASRGSTQIQPSRGFYCIWHDGNOYSACTEPW--TRLNV-----RDKL 413
 Db 527 GICYGSMNRQGP-ESRLGR-----NSASWCVE-WFNTKISAWNNVNEKTLPSKA 574
 QY 414 DKVGVLDYDQGLLIFVN-ADDMSWLYTTRKPPGKLCVSF 453
 Db 575 TRGVLLNCDHGFVIFFAVDKVLHMYKFRVDFTEALYPAF 615

RESULT 13
 I49642
 estrogen-responsive finger protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I49642
 R:Orimo, A.; Inoue, S.; Ikeda, K.; Noji, S.; Muramatsu, M.
 J. Biol. Chem. 270, 24406-24413, 1995
 A:Title: Molecular cloning, structure, and expression of mouse estrogen-responsive finger protein
 A:Reference number: I49642; MUID:96025835; PMID:7592654

Db 461 CLWSS---GK--KPLTI 472

Search completed: July 23, 2004, 15:08:32
Job time : 19 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:04:20 ; Search time 13 Seconds
(without alignments)
1902.563 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELLCSICLSIQD.....GSHANGKNVQLRINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	772	30.8	624	1	A33_PLEWA
2	663.5	26.5	518	1	RN23_HUMAN
3	655.5	26.2	488	1	RN23_MOUSE
4	583	23.3	513	1	RFP_HUMAN
5	580	23.2	522	1	RFP_MOUSE
6	560	22.4	468	1	TM11_HUMAN
7	554.5	22.1	467	1	TM11_MOUSE
8	552.5	22.1	475	1	ROS2_HUMAN
9	550.5	22.0	511	1	TRM7_HUMAN
10	528	21.1	470	1	ROS2_MOUSE
11	505.5	20.2	488	1	TRM6_HUMAN
12	489	19.5	465	1	RN15_HUMAN
13	486	19.4	477	1	TM17_MOUSE
14	475.5	19.0	477	1	TM17_RAT
15	459	18.3	477	1	TM17_HUMAN
16	456	18.2	489	1	RNF9_MOUSE
17	449.5	18.0	482	1	RNF9_HUMAN
18	449	17.9	539	1	Z173_HUMAN
19	448	17.9	539	1	Z173_PANTR
20	444	17.7	481	1	RNF9_PANTR
21	439	17.5	461	1	TM15_PIG
22	430	17.2	465	1	TM15_HUMAN
23	428	17.1	465	1	TM15_PANTR
24	427.5	17.1	781	1	MEFV_HUMAN
25	410.5	16.4	496	1	TM30_MOUSE
26	408.5	16.3	493	1	TRM5_HUMAN
27	372.5	14.9	667	1	MID1_HUMAN
28	369.5	14.8	667	1	MID1_MOUSE
29	362	14.5	680	1	MID1_MOUSE
30	360.5	14.4	667	1	MID1_MOUSE
31	341	13.6	630	1	Z147_HUMAN
32	340.5	13.6	685	1	MID2_MOUSE
33	326.5	13.0	715	1	MID2_HUMAN

34	321.5	12.8	442	1	TM14_HUMAN	Q14142 homo sapien
35	306	12.2	288	1	RFL1_HUMAN	O75677 homo sapien
36	304.5	12.2	634	1	Z147_MOUSE	Q61510 mus musculu
37	301.5	12.0	526	1	BUTY_BOVIN	P18892 bos taurus
38	297.5	11.9	524	1	BUTY_MOUSE	O62556 mus musculu
39	296	11.8	288	1	RFL2_HUMAN	O75678 homo sapien
40	295	11.8	288	1	RFL3_HUMAN	O75679 homo sapien
41	293	11.7	526	1	BUTY_HUMAN	Q13410 homo sapien
42	279.5	11.2	452	1	RN18_HUMAN	Q9ns80 homo sapien
43	276	11.0	425	1	TM31_HUMAN	Q9bzy9 homo sapien
44	269	10.7	551	1	RN27_MOUSE	Q99pj2 mus musculu
45	267	10.7	551	1	RN27_HUMAN	Q9bzy9 homo sapien

ALIGNMENTS

```
RESULT 1
A33_PLEWA
ID_ A33_PLEWA          STANDARD;          PRT;   624 AA.
AC  Q02084;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Zinc-binding protein A33
OS  Pleurodeles waltl (Iberian ribbed newt).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae;
OC  Pleurodeles.
OX  NCBI_TaxID=83119;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Ovary;
RX  MEDLINE=93154311; PubMed=7679068;
RA  Bellini M., Lacroix J.-C., Gall J.-G.;
RT  "A putative zinc-binding protein on lampbrush chromosome loops.";
RL  EMBO J. 12:107-114(1993).
CC  -!- FUNCTION: May be a nuclear regulatory protein that is stored
CC  in the germinal vesicle for use during early embryogenesis
CC  and may play a role in the synthesis or processing of pre-mRNA
CC  during oogenesis.
CC  -!- SUBCELLULAR LOCATION: Nuclear.
CC  -!- DEVELOPMENTAL STAGE: It first appears on the chromosome loops
CC  and in the nucleoplasm of the germinal vesicle (GV). It is
CC  transmitted to the egg at GV breakdown and appears in embryonic
CC  nuclei at the mid-blastula stage and is found in many but not
CC  all nuclei at still later stages of embryogenesis.
CC  -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC  -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC  -!- SIMILARITY: Contains 1 SPRY domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; L04190; AAA49614.1; -.
CC  PIR; S28418; S28418.
CC  InterPro; IPR001870; B302.
CC  InterPro; IPR003649; Bbox_C.
CC  InterPro; IPR006574; PRY.
CC  InterPro; IPR003877; SPRY_receptor.
CC  InterPro; IPR000315; Znf_Bbox.
CC  InterPro; IPR001841; Znf_ring.
CC  Pfam; PF00622; SPRY; 1.
CC  Pfam; PF00643; zf-B_box; 1.
CC  Pfam; PF00097; zf-C3HC4; 1.
CC  SMART; SM00502; BBC; 1.
CC  SMART; SM00336; BBOX; 1.
CC  SMART; SM00589; PRY; 1.
```



```
KW Zinc-finger; Coiled coil; Alternative splicing.
FT ZN_FING 29 70 RING-TYPE.
FT ZN_FING 102 143 B BOX-TYPE.
FT DOMAIN 181 250 COILED COIL (POTENTIAL).
FT DOMAIN 390 515 SPRY.
FT VARSPIC 269 298 Missing (in isoform 2).
FT CONFLICT 137 137 /FTID=VSP 005755.
FT SEQUENCE 518 AA; 59716 MW; DA92B328F25B828 CRC64;

Query Match 26.5%; Score 663.5; DB 1; Length 518;
Best Local Similarity 32.8%; Pred. No. 1.8e-31;
Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;

QY 4 SLKDELLCSICLSIQDPSVSGCEHYFCRCITTEHWVQEAQAGD--CPCCRTFAEPA 61
DB 22 NQVEASCVCLEYLEKEPVITECGHNFCKACITRWEDLE----RDFPCVCRKTSYRS 77

QY 62 LAPSLKLANIVERYSSFPDLAILNARRAARPC-QAHDKVKLFCLTDRLALCFCDPEPALH 120
DB 78 LRPNRQLGSWE--IAKQLQAVKIRDESICPDQHEALSFCYEDQEAVALICAISHTH 135

QY 121 EQHVTGIDDAFDELORELKQALQDSREHTEALQQLKRLAETKSKSLRTTIGE 180
DB 136 RPHTVVPMDDATQYKEKLEQKLEPLEQKLEITCKKASEKKPGELKRLVESRQQLK 195

QY 181 AFERLHRLREROKAMLEELADTARTLTDTIEQKVQYSQOLRVQQAQILQERLAETD 240
DB 196 EFEEHLRRLDEEQQLLSRLEEE-----EQDI-----LQRLRENAHLGDRRRD-- 239

QY 241 RHTFLAGVASISERLKGK-----THEINTLYEDFPTSKYTG-----P 277
DB 240 -----LAHLAEVEGKCIQSGFEMLKDVKSTLEKCEKVKTMETVSVSLEKKNFNP 292

QY 278 LQY-----TIWKSLEFQDIHPVPAALTLDPGTAHQRLILSDDCITIVAYGNLHPQIQDSPKR 333
DB 293 RQYFALRKILKQLIADV-----TLDPETAHPNLVLSSEDRKSKVFTETRLDLPTPQR 345

QY 334 FDEVSVLGSEAFSSGVHYVEVVAETQWVIGLAHAAARKGSIQIOPSRGFYCVIMHD 393
DB 346 FTTPYCVLATEGTSRGRHYVEVEGDKTHWAVGVCRDSVRKGBELTLPETGYWRVLWN 405

QY 394 GNOYSACTEPTWRLNVRDKLVGVFLDQGLIFYNADDMSLWLYTFREKFPCKLCSYF 453

Zinc-finger; Coiled coil; Alternative splicing.
FT ZN_FING 29 70 RING-TYPE.
FT ZN_FING 102 143 B BOX-TYPE.
FT DOMAIN 181 250 COILED COIL (POTENTIAL).
FT DOMAIN 390 515 SPRY.
FT VARSPIC 269 298 Missing (in isoform 2).
FT CONFLICT 137 137 /FTID=VSP 005755.
FT SEQUENCE 518 AA; 59716 MW; DA92B328F25B828 CRC64;

Query Match 26.5%; Score 663.5; DB 1; Length 518;
Best Local Similarity 32.8%; Pred. No. 1.8e-31;
Matches 167; Conservative 85; Mismatches 196; Indels 61; Gaps 13;

QY 4 SLKDELLCSICLSIQDPSVSGCEHYFCRCITTEHWVQEAQAGD--CPCCRTFAEPA 61
DB 22 NQVEASCVCLEYLEKEPVITECGHNFCKACITRWEDLE----RDFPCVCRKTSYRS 77

QY 62 LAPSLKLANIVERYSSFPDLAILNARRAARPC-QAHDKVKLFCLTDRLALCFCDPEPALH 120
DB 78 LRPNRQLGSWE--IAKQLQAVKIRDESICPDQHEALSFCYEDQEAVALICAISHTH 135

QY 121 EQHVTGIDDAFDELORELKQALQDSREHTEALQQLKRLAETKSKSLRTTIGE 180
DB 136 RPHTVVPMDDATQYKEKLEQKLEPLEQKLEITCKKASEKKPGELKRLVESRQQLK 195

QY 181 AFERLHRLREROKAMLEELADTARTLTDTIEQKVQYSQOLRVQQAQILQERLAETD 240
DB 196 EFEEHLRRLDEEQQLLSRLEEE-----EQDI-----LQRLRENAHLGDRRRD-- 239

QY 241 RHTFLAGVASISERLKGK-----THEINTLYEDFPTSKYTG-----P 277
DB 240 -----LAHLAEVEGKCIQSGFEMLKDVKSTLEKCEKVKTMETVSVSLEKKNFNP 292

QY 278 LQY-----TIWKSLEFQDIHPVPAALTLDPGTAHQRLILSDDCITIVAYGNLHPQIQDSPKR 333
DB 293 RQYFALRKILKQLIADV-----TLDPETAHPNLVLSSEDRKSKVFTETRLDLPTPQR 345

QY 334 FDEVSVLGSEAFSSGVHYVEVVAETQWVIGLAHAAARKGSIQIOPSRGFYCVIMHD 393
DB 346 FTTPYCVLATEGTSRGRHYVEVEGDKTHWAVGVCRDSVRKGBELTLPETGYWRVLWN 405

QY 394 GNOYSACTEPTWRLNVRDKLVGVFLDQGLIFYNADDMSLWLYTFREKFPCKLCSYF 453
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DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; Zf-B_Box; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00589; PRY; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00449; SPRY; 1.
DR PROSITE: PS00119; ZF_BBOX; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Zinc-finger; Antigen- RNA-binding; Ribonucleoprotein; DNA-binding.
FT ZN_FING 20 59 RING-TYPE.
FT ZN_FING 96 127 B_BOX-TYPE.
FT DOMAIN 215 236 LEUCINE-ZIPPER.
SQ SEQUENCE 470 AA; 54175 MW; 393AESA5FD254855B CRC64;

Query Match 21.1%; Score 528; DB 1; Length 470;
Best Local Similarity 29.7%; Pred. No. 1.1e-23;
Matches 146; Conservative 87; Mismatches 189; Indels 70; Gaps 18;

QY 7 DELLCSICLSIYQDPVSLGCHYFCRCITTEHWVQEAQAGARDCEPCRTFAEPALAPSL 66
DB 16 EVVTCISICLDPVPEPMSIEGCHFCCKEIFE---VGKNGSGSCPCCQQLLNLRPNR 71
QY 67 KLANIVERYSSPFLDAILNARRARP--COAH-DKVKLFCLTDRALLCFCEDEPALHEQH 123
DB 72 HIANMVENLKQI-----AONTKKSSTQTHCWKGKHLFCEEDGQALCWCAQSGKGRDH 127
QY 124 QVTGIDDAFDELQELKQALQALQDSEREHTEALQL-LKQLAETKSKSLRTTIGFAF 182
DB 128 TRVPEEAQVQEKHVLEKLRKG-KELAEKEMDLTWQTDWNRNDTQKSRHAEF 186
QY 183 ERIHLRLRRKAMLELEADTARTLTIEQKVQRYSQLRKVOEGAQILQERLAETDRH 242
DB 187 ALQNSLLAQEQQLQLEKQDQREYLRLLGKKE-----AELAKNQALQELISELER- 238
QY 243 TFLAGVASLSRLKKG-----IHTNLTYP-----DPPTSKYTG-----LQY 280
DB 239 -----RINGSLELLOEVRILERSGSWNLDITDIDAPDLTSTCPVGRKKMLR 287
QY 281 TIWKSFLQIHVPVPAALTDPGTAHQRLILSDCTTIVAGNLHPQLQSPKRFDEVSU 340
DB 288 TCW-----VH-----ITLDRTANSWLILSKDRQVRMGDTH-QNVSDNKERFSNPMV 335
QY 341 LGSEAFSSGVHVVVVAEKTOVIGLAHEAASRKSGIQIPSGRGFYCIVMHDGNOYSAC 400
DB 336 LGAQRFSSGKMYWEVDVTKQEAWDLGVRDVSQKGFQSLSPENGFWTIWLQ-DSYEAG 394
QY 401 TEPWTLNVRDKLDKGVFLVDYDQGLLIIFYN-ADDMSNLYTFPE-KFPGKLCYSFPGQS 458
DB 395 TSPQTTLHTQVPPCIGIFVDYEAGVVSFYNTIDHGSLIYTFSECFVAGLRPFNVGN 454
QY 459 HANGKNVQPLRI 470
DB 455 YSGG-NAAPKL 465

RESULT 11
ID TRM6 HUMAN STANDARD; PRT; 488 AA.
AC Q9C030;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tripartite motif protein 6.
GN TRIM6.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```

Db 179 ERRIQTFNQRLNDRVQREKLEQBEKKGLRIIEEAENDLVHQTQSLRELISDL- 237
Qy 234 ERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGPIQYTIWKSLEFQ- 288
Db 238 ERRCQGSTMEILLQDVSDYTER-----SEFWTLRKPEALP-TKLRSMPFRAPDLK 284
Qy 289 -----DIHFVPAALTLDPGTAHORLLISDCTTIVAYGNLHPQLQSPKRFVVEV 338
Db 285 RMLRVCRELTVDQSVXWVDVTLNPHITANLVLAKNRQRFVFGAKVSPSCLEKHYD--C 342
Qy 339 SVLGEAEFSSGVHYWEVVAEKTOWVIGLA-----HEAASRKGSIQIOPSRGEY 387
Db 343 SVLGSQHESSGKHVEVDVAKTAWILGVCSNLGPTSFNHFQNHSAIRYQDSQYIW 402
Qy 388 CIVMHGNGQYAC--TEPTWRLNVRDKLVGVFLDYDQGLLIIFYNADMSW-LYTF-RE 443
Db 403 VIGLQNHXYRAYEDSSPLLISMTVPRRVGVFLDYEAGTVSFYVNTNHHGFFIYTFSKY 462
Qy 444 KFGKLCYSFSP 455
Db 463 YFPTTLCYFNP 474

RESULT 12
RN15_HUMAN
ID RN15_HUMAN STANDARD; PRT; 465 AA.
AC O00635;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RING finger protein 15 (Zinc finger protein Rofet) (Tripartite motif-
DE containing protein 38).
GN TRIM38 OR RNFI5 OR RORET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97294057; PubMed=9149941;
RA Ruddy D.A., Kromal G.S., Lee V.K., Mintier G.A., Quintana L.,
RA Domingo R. Jr., Meyer N.C., Irinkki A., McClelland E.E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RA "A 1.1-Mb transcript map of the hereditary hemochromatosis locus.";
RL Genome Res. 7:441-456(1997).
RN [2]
SEQUENCE FROM N.A.
RX TISSUE=Lung;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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```

CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -!- SIMILARITY: Contains 1 SPRY domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U91328; AAB82084.1; -.
DR EMBL; U90547; AAB53425.1; -.
DR EMBL; BC026930; AAB26930.1; -.
DR Genew; HGNC:10059; TRIM38.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Box.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS01119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Zinc-finger; Polymorphism.
FT ZN_FING 16 63 RING-TYPE.
FT ZN_FING 88 129 B_BOX-TYPE.
FT DOMAIN 344 464 SPRY.
FT VARIANT 421 421 G -> R (in dbSNP:8469041).
FT /FTID=VAR_013513.
FT CONFLICT 23 23 M -> I (IN REF. 2).
FT /FTID=VAR_013513.
SQ SEQUENCE 465 AA; 53416 MW; 30A884051A2DA058 CRC64;

Query Match 19.5%; Score 489; DB 1; Length 465;
Best Local Similarity 29.3%; Pred. No. 2e-21;
Matches 137; Conservative 79; Mismatches 207; Indels 44; Gaps 11;

Qy 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCITTEHWROEAGARD-----CEECRTFAEP 60
Db 10 MMEFATCSICLSLMTNPFVINCCHSYCHLCITDFFKNPSQKLRQETCCQCRAPFMD 69
Qy 61 ALAPSLKLANIVERYSPFLDAILNARRAAPCOAH-DVKLFLCLTDRLALCFCEDEPAL 119
Db 70 SLRPNKQLGSLIE-----ALKETDQMSCEHGEQFHLFCEDEQLICWCERAPQ 120
Qy 120 HEQHQVTGIDDAFDELQRELKQALQDSREHTEALQLKRLQLAETKSTKSLRTTIG 179
Db 121 HKGHTTALVEDVCQYKELQKAVTKLQLEDRCQKLTAMRITKWKVKVQIQRKIR 180
Qy 180 EAFELHRLLEEROKAMELEEAETARTLT---DIEQKVQRYSQQLR-----KVQEG 228
Db 181 SDFKNQLQCFLEHEEKSYLWLRKEEQQLTSLRDYEAAGLGLKSNELKSHILEBEKCGS 240
Qy 229 AQILOERLAETDRHTFLAGVASLSERLKGKIHETNLTYEDFTSKYTGPIQYTIWKSLEFQ 288
Db 241 AQKLLQNVNDT-----LSRSWAVKLETSEAVSLELHTWCNVSKLYFDVKKMLRS 289
Qy 289 DIHPVPAALTLDPGTAHORLLISDCTTIVAYGNLHPQLQD-SPKRFVDEVSVLGSEAFS 347
Db 290 --HQV--SVTLDPDTAHELILSEDRRQVTRG--YTQENQDTSRRRTFAFPVLCGCEGT 343
Qy 348 SCVHYWEVVAEKTQWVIGLAHEAASRKGSIQIOPSRGFYCIVMHNGNQYACTEPTWRL 407
Db 344 SGRFYEVDFVGEGTGWDVLGVCMENVGRTGKMQPQSGFWTLRLCKKGYVALTSPPTSL 403
Qy 408 NVRDKLDKGVFLDYDQGLLIIFYNADMSWLYTF-REKFPGLKCSYF 453

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404 HLHEQPLLVGIFLDVAGVVSFNGTGCCHITFFPKASFSDLRPYF 450

RESULT 13

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TM17_MOUSE
ID TM17_MOUSE STANDARD; PRT; 477 AA.
AC Q7TEM3; Q99PP8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tripartite motif protein 17.
GN TRIM17.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testicle; PubMed=12477932;
RX MEDLINE=2398257;
RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE OF 383-477 FROM N.A.
RX MEDLINE=21231161; PubMed=11331580;
RA Raymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
RA Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanci A.,
RA Minucci S., Pelicci P.G., Ballabio A.;
RT "The tripartite motif family identifies cell compartments.";
RL EMBO J. 20:2140-2151(2001).
CC -!- TISSUE SPECIFICITY: Almost exclusively in the testis.
CC -!- SIMILARITY: Belongs to the TRIM/RBCC family.
CC -!- SIMILARITY: Contains 1 B30.2-like domain.
CC -!- SIMILARITY: Contains 1 B box-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BC055112; AAH55112.1; -
CC EMBL; AF220135; AAG53508.1; -
CC MGD; MGI:1861440; Trim17.
CC InterPro; IPR001870; B302.
CC InterPro; IPR006574; PRY.
CC InterPro; IPR003877; SPRY receptor.
CC InterPro; IPR000315; Znf_Ebox.
CC InterPro; IPR001841; Znf_Ring.
CC Pfam; PF00622; SPRY; 1.
CC Pfam; PF00643; zf-B_box; 1.
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DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRI; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS01119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Coiled coil; Zinc-finger.
FT ZN FING 16 66 RING-TYPE.
FT ZN FING 94 135 B BOX-TYPE.
FT DOMAIN 135 226 COILED COIL (POTENTIAL).
FT DOMAIN 297 456 B30.2-LIKE.
SQ SEQUENCE 477 AA; 54863 MW; E05066304224AAE CRC64;
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Query Match 19.4%; Score 486; DB 1; Length 477;

Best Local Similarity 28.4%; Pred. No. 3e-21;

Matches 140; Conservative 83; Mismatches 194; Indels 76; Gaps 17;

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QY 1 MACSLKDELLCSICLSIYODPVSLGCEHYFCRCITEHWV-----ROEAQAGDCPEC 53
DB 6 LARRIQEEATCSICLDYFTDPWTACGHNFCRECIOMSEKVKVKKQKGSFFCPEC 65
QY 54 RTFAEPALAPSLKLANIVERYSSFPDLAILNARRAARPCQAH-DKVKLFCLTDRALLCF 112
DB 66 REMSPQRNLRPNRLTKVAEMARQHP-----GLQKRDLCQAHQEPLKLFCDQDQSPICV 119
QY 113 FDEPALHQHQVQTGIDDAFDELQRELKQALQDSEREHTALQLLKRO-LAETKSST 171
DB 120 VCREAQEHMRHVRVLPIDEAAREYKLEEDIKYLR-EMMKTTETLOAKEQITLWQERV 178
QY 172 KSLRTTIGAFERLHLLREROKAMLEEL---EADTARTLTDEQKVQVYSQOL----- 222
DB 179 KERRERILEEFQKRVLFVEERRILQVJLKKKEEDTLGKLQSKASLDHQSRSLDILLQ 238
QY 223 ---RKVQGAQILQERLAETDRHTFLAGVASLSERLKGKIHNLTLYED--PFTSKYT-- 275
DB 239 LEERSQEQEQLMLQD-----VKDTLNRK-ESFSVQYPEVWLPAIKTLCL 281
QY 276 -GPLQVTIWSKLFQDIHPVPAALTDPGTAHQRLILSDCTIVAYGN-----LHPQLQD 329
DB 282 RVFGQIEVLKSFQEDYMP-----DPSAYFYLL-----YESRQRYLSPFPPEG 326
QY 330 SP---KRPDVEVSLGSEAFSSGVHYEV--VVAEKTQWVIGLAHEAASRGSIQIOPSR 384
DB 327 AYSKDRFVAYPCAVQCKSFSSGRHYWEVOMLTGALWALGVCRNVSRKDRVLKSPEN 386
QY 385 GFYCIYMHGDNQVSACTEPTWRLNVRDKLDKVGFLDYPDQGLLIFYNADDMWLYTFRE- 443
DB 387 GEVWVQLSKGKQLSLPNSTLVLTPEPSHMGIFLDFQAGEVFSYVNDGSHLSFSQA 446
QY 444 KFPGLKCSYFSPG 456
DB 447 AFPGLLPFFCLG 459
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RESULT 14

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TM17_RAT
ID TM17_RAT STANDARD; PRT; 477 AA.
AC Q9WV59;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tripartite motif protein 17 (Testis RING finger protein).
GN TRIM17 OR TERF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=testis;
RX MEDLINE=99011410; PubMed=9792805;
```


DR EMBL: AF156271; AAD40286.1; -;
DR EMBL: EC033788; AAH33788.1; -;
DR Genew; HGNC:13430; TRIML7;
DR MIM; 606123; -;
DR InterPro; IPR001870; B302.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; ZF-B-box; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR PROSITE; PS00119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Coiled coil; Zinc-finger.
FT ZN FING 16 66 RING-TYPE.
FT ZN FING 94 135 B_BOX-TYPE.
FT DOMAIN 135 223 COILED COIL (POTENTIAL).
FT DOMAIN 297 456 B30.2-LIKE.
SQ SEQUENCE 477 AA; 54418 MW; ECA4010661ADD28A CRC64;

Query Match 18.3%; Score 459; DB 1; Length 477;
Best Local Similarity 27.0%; Pred. No. 1.1e-19;
Matches 130; Conservative 85; Mismatches 214; Indels 52; Gaps 12;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWV-----RQEAQAGDCPEC 53
Db LARKIQEATCSICLDYFDPTWTTTCGHNFACQLSWEKARGKGRKRKSGFPCEC 65

QY 54 RTFAEPALAPSLKLANIVERYSSPFLDALNARARPCQA-HDKVKLFCLTDRALLCF 112
Db REMSPQRNLLPNRLTKVAEMAQHP-----GLQKQDLCOEHPELKLFCCKQDSPICV 119

QY 113 FODEPALHEQHVTDGIDDAFDELQRELQALQDSEREHTEALQLKRO-LAETKST 171
Db VCRESEHRLHRLVPAEEAVQGYKLEEDMEYLRE-QITRTGNLQARBEQSLAEWQGV 178

QY 172 KSLRTTIGAFERLHLEROKAMLELEADTARTLTDIEQV-----QRYSQQLRKVQ 226
Db KERRERIVLEFKMNLVLEEQRLLQALETEETASRLRESVACLDRQHSLELLIQ 238

QY 227 EGAQILQERLAETDRHTFLAGVASLSERLKGKHETNLTYEDPFTSKYTGPIQYTIWKS 286
Db -----LEERSTQGLQMLQDMKEPLSRKKNVSVQCEVAPPTPRIVCRVPGIEVLRGF 293

QY 287 FODIHPVPAALVLDGTAHQRLILSDDCITIVAGNLHPQLQDSPK-----RPDVEV 338
Db LEDVVP-----DATSAYPYLL-----YESRRYLGSSPEGSGFCSKDRFVAYP 338

QY 339 SVLGSEAFSSGVHYWEV--VVAEKTQWIGLAHEAASRKSGSIQPSRGFYCIWMHDGNO 396
Db CAVGQTAFSSGRHYVEVGNNITGDALWALGVCRDENVSRKDRVPKCPENGFWVQISKGTK 398

QY 397 YSACTEPWTRLNVRDKLDVGVFLDYDQGLLIFYNADDMSWLYTPRE-KPPGKLCSYFSP 455
Db YLSTFSALTPVMLMEPPSHMGIFLDFEAGEVSFYSVSDGSHLHTYSQATFPGLQPPFFCL 458

QY 456 G 456
Db 459 G 459

Search completed: July 23, 2004, 15:08:04
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 15:03:50 ; Search time 42 Seconds
(without alignments)
3568.361 Million cell updates/sec

Title: US-09-927-091-1

Perfect score: 2504

Sequence: 1 MACSLKDELICSLSIYQD.....GQSHANGKNVQPLINTVRI 475

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25; *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2504	100.0	475	4	Q9BVG3	Q9bv93 homo sapien
2	2491	99.5	475	4	Q9NVG0	Q9nv93 homo sapien
3	2491	99.5	475	11	Q80V85	Q80v85 mus musculus
4	763.5	30.5	609	13	Q92021	Q92021 xenopus lae
5	748.5	29.9	610	13	Q91431	Q91431 xenopus lae
6	693.5	27.7	453	13	Q80IR9	Q80ir9 xenopus lae
7	664.5	26.5	496	11	Q8K0F7	Q8k0f7 mus musculus
8	662.5	26.5	488	4	Q8IYT9	Q8iyt9 homo sapien
9	638.5	25.5	479	13	Q7ZU70	Q7zu70 brachydanio
10	619	24.7	500	4	Q86WT6	Q86wt6 homo sapien
11	603.5	24.1	500	11	Q80X56	Q80x56 mus musculus
12	599.5	23.9	500	11	Q8VH26	Q8vh26 mus musculus
13	593	23.7	483	11	Q81012	Q81012 mus musculus
14	588	23.5	483	11	Q81011	Q81011 rattus norv
15	581	23.2	486	6	Q865W2	Q865w2 sus scrofa
16	577	23.0	513	11	Q8C2Q5	Q8c2q5 mus musculus

17	576	23.0	486	4	Q86XT3	Q86xt3 homo sapien
18	576	23.0	513	11	Q99LK1	Q99lk1 mus musculus
19	575.5	23.0	487	4	Q86XT4	Q86xt4 homo sapien
20	572	22.8	506	11	Q62157	Q62157 mus musculus
21	553.5	22.1	483	11	Q8VDX5	Q8vdx5 mus musculus
22	550.5	22.0	485	4	Q96PF7	Q96pf7 homo sapien
23	550.5	22.0	485	4	Q8WZ70	Q8wz70 homo sapien
24	550.5	22.0	511	4	Q96J90	Q96j90 homo sapien
25	540.5	21.6	469	6	Q7YRV4	Q7yrv4 bos taurus
26	529	21.1	470	11	Q921V6	Q921v6 mus musculus
27	523.5	20.9	485	11	Q8K243	Q8k243 mus musculus
28	520	20.8	501	11	Q8BVY9	Q8bvy9 mus musculus
29	520	20.8	501	11	Q8VID4	Q8vid4 mus musculus
30	520	20.8	514	11	Q810V7	Q810v7 mus musculus
31	520	20.8	516	11	Q8C006	Q8c006 mus musculus
32	516	20.6	486	11	Q7TQL7	Q7tql7 mus musculus
33	513	20.5	470	11	Q8BVP1	Q8bvp1 mus musculus
34	505.5	20.2	516	4	Q86WZ8	Q86wz8 homo sapien
35	501	20.0	471	4	Q8NA35	Q8na35 homo sapien
36	500	20.0	468	4	Q8N9V2	Q8n9v2 homo sapien
37	494	19.7	514	13	Q800L5	Q800l5 anguilla ja
38	486	19.4	477	11	Q7TEM3	Q7tpm3 mus musculus
39	483	19.3	493	4	Q86XQ0	Q86xq0 homo sapien
40	483	19.3	504	4	Q9UPQ4	Q9upq4 homo sapien
41	480.5	19.2	341	4	Q81YX3	Q81yv3 homo sapien
42	475.5	19.0	477	11	Q9WV59	Q9wv59 rattus norv
43	459	18.3	477	4	Q9Y577	Q9y577 homo sapien
44	458.5	18.3	296	4	Q8WY17	Q8wyl7 homo sapien
45	456	18.2	489	11	Q80WA9	Q80wa9 mus musculus

ALIGNMENTS

RESULT 1

Q9BVG3					
ID	Q9BVG3	PRELIMINARY;	PRT;	475 AA.	
AC	Q9BVG3;				
DT	01-JUN-2001 (TrEMBLrel. 17, Created)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye;				
RA	Strausberg R.;				
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				
DR	EMBL; BC001222; AAH01222.1; -				
DR	EMBL; BC012152; AAHL2152.1; -				
DR	EMBL; BC007999; AAH07999.1; -				
DR	EMBL; BC011689; AAHL1689.1; -				
DR	GO; GO:0005622; C:intracellular; IEA.				
DR	GO; GO:0008270; F:zinc ion binding; IEA.				
DR	InterPro; IPR001870; B302.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR006574; PRY.				
DR	InterPro; IPR003877; SPKv_receptor.				
DR	InterPro; IPR000315; Znf_Box.				
DR	Pfam; PF00622; SPRY; 1.				
DR	Pfam; PF00643; zf-B_box; 1.				
DR	Pfam; PF00097; zf-C3HC4; 1.				
DR	SMART; SM00589; PRY; 1.				
DR	SMART; SM00184; RING; 1.				
DR	PROSITE; PS00290; IG_MHC; 1.				
DR	PROSITE; PS00119; ZF_Box; 1.				
DR	PROSITE; PS00518; ZF_RING_1; 1.				
DR	PROSITE; PS00089; ZF_RING_2; 1.				

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54267 MW; DC15CA9B795DEBB0 CRC64;

Query Match 100.0%; Score 2504; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.1e-160;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQOARDCEPCRRTFABP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQOARDCEPCRRTFABP 60
QY 61 ALAPSLKLANIYERYSSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFCDPALH 120
DB 61 ALAPSLKLANIYERYSSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFCDPALH 120
QY 121 EHQVGTGDDADEFQRELKQDLQALQDSERHEALQLLKRQAEKSTKSLRTTIGE 180
DB 121 EHQVGTGDDADEFQRELKQDLQALQDSERHEALQLLKRQAEKSTKSLRTTIGE 180
QY 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQQLRKVOEGAIQERLAETD 240
DB 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQQLRKVOEGAIQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTVEPPTSKYTGPLYTIWKSFLQDHPVPAALTLD 300
DB 241 RHTFLAGVASLSERLKGKIHETNLTVEPPTSKYTGPLYTIWKSFLQDHPVPAALTLD 300
QY 301 PGTARQLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
DB 301 PGTARQLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
QY 361 TQWVIGLAHEAASRKSGIOIQSRGFYCIWMDGNQYSACTEPWTLNVRDKLDKVGVEL 420
DB 361 TQWVIGLAHEAASRKSGIOIQSRGFYCIWMDGNQYSACTEPWTLNVRDKLDKVGVEL 420
QY 421 DYDQGLLIIFYNADMSWLYTFREKPKGLCSYFSPGQSHANGKNVQPLINTVRI 475
DB 421 DYDQGLLIIFYNADMSWLYTFREKPKGLCSYFSPGQSHANGKNVQPLINTVRI 475

RESULT 2

Q9NVG0 PRELIMINARY; PRT; 475 AA.
AC Q9NVG0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ10759.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuko Y., Kanehori K.;
RT "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AK001621; EAA91792.1; -!
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; Zf-B_box; 1.

DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 475 AA; 54150 MW; 7C04489D3B5C0F6C CRC64;

Query Match 99.5%; Score 2491; DB 4; Length 475;
Best Local Similarity 99.6%; Pred. No. 8.4e-160;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQOARDCEPCRRTFABP 60
DB 1 MACSLKDELLCSICLSIYQDPVSLGCEHYFCRCITEHWVROEAQOARDCEPCRRTFABP 60
QY 61 ALAPSLKLANIYERYSSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFCDPALH 120
DB 61 ALAPSLKLANIYERYSSFFLDAILNARRAARPCQAHDKVKLFCLTDRLALLCFCDPALH 120
QY 121 EHQVGTGDDADEFQRELKQDLQALQDSERHEALQLLKRQAEKSTKSLRTTIGE 180
DB 121 EHQVGTGDDADEFQRELKQDLQALQDSERHEALQLLKRQAEKSTKSLRTTIGE 180
QY 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQQLRKVOEGAIQERLAETD 240
DB 181 APERLHRLREROKAMLELEADTARTLTDIEQVORYSQQLRKVOEGAIQERLAETD 240
QY 241 RHTFLAGVASLSERLKGKIHETNLTVEPPTSKYTGPLYTIWKSFLQDHPVPAALTLD 300
DB 241 RHTFLAGVASLSERLKGKIHETNLTVEPPTSKYTGPLYTIWKSFLQDHPVPAALTLD 300
QY 301 PGTARQLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
DB 301 PGTARQLILSDCTIVAYGNLHPQLQSPKRFDEVSVLGSEAFSSGVHVEVVAEK 360
QY 361 TQWVIGLAHEAASRKSGIOIQSRGFYCIWMDGNQYSACTEPWTLNVRDKLDKVGVEL 420
DB 361 TQWVIGLAHEAASRKSGIOIQSRGFYCIWMDGNQYSACTEPWTLNVRDKLDKVGVEL 420
QY 421 DYDQGLLIIFYNADMSWLYTFREKPKGLCSYFSPGQSHANGKNVQPLINTVRI 475
DB 421 DYDQGLLIIFYNADMSWLYTFREKPKGLCSYFSPGQSHANGKNVQPLINTVRI 475

RESULT 3

Q8OV85 PRELIMINARY; PRT; 475 AA.
AC Q8OV85;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN cDNA 6330414G21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

[illegible][illegible]

RESULT 4

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QY 243 TEL----AGVASLSRLKGIHETN-LTYEDPSTKYTGPLYTINKSLFQDIHPVPAAL 297
Db 375 SELMDIKAFIDKQEQORAVISTGNTLLSKELCOGTFKGPIQIYIMMKELKSVVIPSITPM 434
QY 298 TLDPGTAHQRLILSDCTIVAYGNLHPQPLQSPKRFDEVSVLGSEAFSSGVHYWEVVV 357
Db 435 LLDPTSAPNLHLSDGLTSRYGE-NKLSLPDNPFRFSQCILVLGSGFDSGRHYWEV 493
QY 358 AKETQWVIGLAHAARKGSIQIOPSRGFCYIWMHDGNOYSACTEPWTRINVRDKLDKVG 417
Db 494 GOKTAMDVGWASESSNRKGIKLPKNKGWAIWLRNGNAYKALESPSKLSLSSHPKXIG 553
QY 418 VFLDYDQGLLIIFYNADMSWLYTFREKFPKGLCSYSPGOSHANGKNVPLR 469
Db 554 VYVDYEGGQISFYNADMTIIYFNATFTTEKLYPLSP-FLHDSGRKNVDPLR 604

RESULT 5
Q91431
ID Q91431 PRELIMINARY; PRT; 610 AA.
AC Q91431;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nuclear factor 7.
GN XNF7-O.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96081373; PubMed=8541218;
RA Gong S.G., Reddy B.A., Etkin L.D.;
RT "Two forms of Xenopus nuclear factor 7 have overlapping spatial but
RT different temporal patterns of expression during development.";
RL Mech. Dev. 52:305-318(1995).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; S80988; AAB35876.1; -.
DR GO; GO:000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:003682; F:chromatin binding; IEA.
DR GO; GO:008270; F:zinc ion binding; IEA.
DR GO; GO:008333; P:chromatin assembly/disassembly; IEA.
DR InterPro; IPR01870; B302.
DR InterPro; IPR003649; Bbox C.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00298; CHROMO; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS0119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 610 AA; 69115 MW; D828F60060572EC1 CRC64;

Query Match 29.9%; Score 748.5; DB 13; Length 610;
Best Local Similarity 33.4%; Pred. No. 3.3e-42;
Matches 159; Conservative 94; Mismatches 198; Indels 25; Gaps 8;

QY 7 DELLCSICSIYQDPVSLGCEHYFCRCITTEHWVROEAQGARDPCRCRTFAEPALAPSL 66
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Db 142 BELTCLVCLVELKDPVWACGHNFCSIDKW---EGQSSPACPECKSITDRKYTINR 198
QY 67 KIANIVERYSSPFLDAILNARRAARCOAHD-KVKLFCLTDRALLCFDEPALHBOHQV 125
Db 199 VLANLAKAACTVTVPEKKTRPLEKCSERHERLKLKYCKDDGTGCVICRDSLKHASHNF 258
QY 126 TGIDDAFDELQRE-----LKQQLAQDSEREHEATEALQLKRLAETKSSITSLRTTI 178
Db 259 LPILDAIGVYRELSAIVAPLEASLVKTEQLSGQSDKIEQHNNKNSVQYKEHWTS----- 313
QY 179 GRAFERLRLRLRRQKAMLEELFADTARTLTIDIEQKVQRYSQQLRVQGAQILQRLAE 238
Db 314 --EFEKHLKFLKEREKLEQLKEQGNLLTTEMNNLVKMQENQDAIKTISLAKERMEE 371
QY 239 TRHTPLAGVASL-----SERLKGKIHTN-LTYEDPSTKYTGPLYTINKSLFQDIHPV 293
Db 372 TDSISFLTIDIKTFDKCQEQORAVISTGNTLLSKELCOGTFKGPIQIYIMMKELKSVITPS 431
QY 294 PAALTLDPGTAHQRLILSDCTIVAYGNLHPQPLQSPKRFDEVSVLGSEAFSSGVHYW 353
Db 432 LTPMLLDPSAHNLHLSDGLTSRYGE-NKLSLPDNPFRFSQCILVLGSGFDSGRHYW 490
QY 354 EVVVAEKTQWVIGLAHAARKGSIQIOPSRGFCYIWMHDGNOYSACTEPWTRINVRDKL 413
Db 491 EVEVGDKTAMDVGWASESSNRKGIKLPKNKGWAIWLRNGNRYKALESPSKALSLSHP 550
QY 414 DKGVFVLDYDQGLLIIFYNADMSWLYTFREKFPKGLCSYSPGOSHANGKNVPLR 469
Db 551 RKIGVYVDYEGGQISFYNADMTIIYFNATFTTEKLYPLSP-FLHDSGRKNVDALR 605

RESULT 6
Q801R9
ID Q801R9 PRELIMINARY; PRT; 453 AA.
AC Q801R9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047956; AAH47956.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR003649; Bbox C.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS0119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 453 AA; 51318 MW; B7D93755706B5406 CRC64;

Query Match 27.7%; Score 693.5; DB 13; Length 453;
Best Local Similarity 33.1%; Pred. No. 1.1e-38;
```


OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Brain;	
RA	Strausberg R.;	
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC047945; AAH47945.1; -.	
DR	InterPro; IPR001870; B302.	
DR	InterPro; IPR006574; PRY.	
DR	InterPro; IPR003877; SPRY receptor.	
DR	InterPro; IPR001841; Znf_Ring.	
DR	Pfam; PF00622; SPRY; 1.	
DR	Pfam; PF00097; ZF-C3HC4; 1.	
DR	SMART; SM00589; PRY; 1.	
DR	SMART; SM00184; RING; 1.	
DR	SMART; SM00449; SPRY; 1.	
DR	PROSITE; PS00518; ZF_RING_1; 1.	
DR	PROSITE; PS00089; ZF_RING_2; 1.	
SQ	SEQUENCE 500 AA; 57448 MW; 0108A705BD03FDE1 CRC64;	
Query Match		
Best Local Similarity 31.8%; Pred. No. 1.3e-33;		
Matches 149; Conservative 83; Mismatches 221; Indels 16; Gaps 8		
QY	8 ELLCSICLSIYQDPVSLGCEHYFCRCITEHWVRQEAQARDCEPCRTFAEPALAPSUK 67	
Db	38 ELHCPLCNDWFRDPLMLSCGHNFCEACIQDFWRLQAKE--TPCECKMLCYNNCTFNPV 95	
QY	68 LANTVERYSFPDLAINNARARCOAH-DKVKLFCITDRALLCFCDPEPALH--EQHQ 124	
Db	96 LDKUVEKIKKPL-----LKGHPQCPPEHGENLKLFSKPDGKLI CFQCKDARLSVGQSKE 149	
QY	125 VTGIDDAFDELQRELKQLOALQDSEREHTEALQLLKQLAETKSTSLRTTICEAFER 184	
Db	150 FLQISDAVHFFMEELAIQOQLETTLKELQTLRNMQKAIAAHKENKHLHQHVSMEFLK 209	
QY	185 LHRLLRERQKAMLEBEADTARTLTIDIQKVRYSQQLRKVQEGAQIILQERLAETDRHTF 244	
Db	210 LHQFLHSKEKDILTRELREGKALNEEMELNLSQLEQCLLAKDMLVSIQAKTEQQNSDFD 269	
QY	245 LAGVASLSERLKG--KIHET-NTLYDEDPSTKYTCPLQYTTWKSLFQDIHPVPAALTLD 301	
Db	270 LKDITTLHLSLEQGMKVLATRELRSKLNQKGKGIQYMWVREMDTLCPLSLPTLDP 329	
QY	302 GTAQRRLISDDCTIVAGNLHPQLQDSKPRFDVEVSVLGEAFSSGVHYWVVAEKT 361	
Db	330 KTAHPNLVLSKQTSVWHGDI-KKIMPPDPERFDSSVAVLSRGFTSGKWTWEVEVAKT 388	
QY	362 QWVTGLAHEAASRKSGSIQIOPSRGFYCIYVMDHGNQYSACTEPWTRLNVRDKLDKGVFLD 421	
Db	389 KWTGVGVRESIIRKSGCPLTPEQGFLLRLRNQTDLKALDLPFSFLTTLNNLDKGVLYD 448	
QY	422 YDQGLLIIFYNADMSLWLYTFREKPPGKLCVSFPGQSHANGKNVQPLRI 470	
Db	449 YEGQLSFYNAKTHTHTYTSNTFMKELPYFPCPLND-GGENKEPLHI 496	
RESULT 11		
Q80X56	PRELIMINARY; PRT; 500 AA.	
ID	Q80X56	
AC	Q80X56;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Ring finger protein 36.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testicle;	
RX	MEDLINE=22388257; PubMed=12477932;	

RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Ditachenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettunen M., Madan A.C., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalius D.E., Schmerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISUE=resticlc;
RA	Strausberg R.;
RL	Submitted (APR-2003) to the EMBL/GenBank/DDJ databases.
DR	EMBL; BC050815; AAH50815.1; --
DR	InterPro; IPR001870; B302.
DR	InterPro; IPR006574; PRY.
DR	InterPro; IPR003877; SPRY receptor.
DR	InterPro; IPR001841; ZnF Ring.
DR	Pfam; PF00622; SPRY; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00589; PRY; 1.
DR	SMART; SM00184; RING; 1.
DR	SMART; SM00449; SPRY; 1.
DR	PROSITE; PS00518; ZF RING 1; 1.
DR	PROSITE; PS00089; ZF RING 2; 1.
SQ	SEQUENCE 500 AA; 57312 MW; 607B0CEB02213754 CRC64;
Query Match	24.1%; Score 603.5; DB 11; Length 500;
Best Local Similarity	31.1%; Pred. No. 1.5e-32;
Matches 152; Conservative	82; Mismatches 205; Indels 49; Gaps 11
Qy	5 LKDELLCSICLSIYODPVSIGCEHYFCRCCTEHVWROEAQGARDPCBCRRFFAFPALAP 64 : : : : : : : : : : : : : : :
Db	36 LTTEHGPLCNDWFDPMLTFCGNFCODCIQSFWKHSHKE--TFPCDCXMKCYSNCTFP 93 : : : : : : : : : : : : : : :
Qy	65 SLKLANIVERYSSPFDLAILNARAAARPQAH-DKVKFLCLTDRLALGCFCDPEALHEQH 123 : : : : : : : : : : : : : : :
Db	94 NLVLEKLVEKIKLPL-----LKGHQPCEHGENLKFSPGEKWIFCKDKARLS--- 144 : : : : : : : : : : : : : : :
Qy	124 QVTGIDAFDELQRELKDQALQDSREHTETALQLKRQIAETSKTSKSLRTTGEEA-- 181 : : : : : : : : : : : : : : :
Db	145 -----MGQSKDFLO-ISEAVRFTEELAIYQSOLQTTLKELQSLRTIQKDAIS 191 : : : : : : : : : : : : : : :
Qy	182 -----FERHLIRERQKAMLEEADTARTLTIDEKVQRYSQLRKV 225 : : : : : : : : : : : : : : :
Db	192 AYDNKTKLQONLSLEFKLHFQHNKEKOILNLRDEGLLNBEVNLNQIQEOCLVA 251 : : : : : : : : : : : : : : :
Qy	226 QEQAIIQLERLAETDRHTFLAGVASLSERL-KG--KIHTNTLYTDFDFTSKVTGLPYIT 282 : : : : : : : : : : : : : : :
Db	252 KDMLATIQAARMQQNSFDLTDITLKIESMEKGMTIVPRQLIAKLSLGREFGIQYII 311 : : : : : : : : : : : : : : :
Qy	283 WKSLFQDIHPVPAAALTDPGTANHQRLLISDDCTTVAYGNLHPQIPQDSPKRFDVSVVG 342 : : : : : : : : : : : : : : :
Db	312 WKEMQAILSPGPSOLLTPDKTAHPNLVLNLSKQTSVCHCDV-QVMPPDPERFDDSSVAVLG 370 : : : : : : : : : : : : : : :
Qy	343 SEAFSSGVHWYEVVAEKTOVIGLAHEAASRKSGIQPSRGFYCIYVHDNGQYSACTE 402 : : : : : : : : : : : : : : :
Db	371 SKGFTSGKWYEIEVGKKTKWTICGVRESIIRKSGSCPLTPQGGFWLLRLRQTDLKALDL 430 : : : : : : : : : : : : : : :
Qy	403 PWTRLNVNRDKLDKVGVDLYDQGLLIIFYNADDMSWLTYFREKFGPKLCYFSFGOSHANG 462 : : : : : : : : : : : : : : :

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DB 431 PRRSLTGLD-LRRVGVLDYEGGQVSYFNATTMTHTLTYTSSVFOEKLFPYLCPCLND-GG 488
QY 463 KNVQPLRI 470
DB 489 ENKEPLHI 496

RESULT 12
Q8VHZ6 PRELIMINARY; PRT; 500 AA.
AC Q8VHZ6;
DT 01-WAR-2002 (TREMELrel. 20, Created)
DT 01-WAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-WAR-2003 (TREMELrel. 23, Last annotation update)
DE Ring finger-B box-coiled coil transcription factor.
GN RNF36.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=21463391; PubMed=11578878;
RX Shyu H., Hsu S., Hsieh-Li H., Li H.;
RT "A novel member of the RBCC family, Trif, expressed specifically in
RT the spermatids of mouse testis.";
RL Mech. Dev. 108:213-216 (2001).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF334958; AAL41031.1; --
DR MGD; MGI:1918178; Rnf36.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 500 AA; 57234 MW; 757907426D8A4E27 CRC64;

Query Match 23.9%; Score 599.5; DB 11; Length 500;
Best Local Similarity 31.1%; Pred. No. 2.8e-32;
Matches 152; Conservative 81; Mismatches 206; Indels 49; Gaps 11;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRRCCITEHHVVRQEAQAGDCEPCRRRTFAEPALAP 64
DB 36 LTTELHCPCLNDWFRDPLMTGCHNFCQDCIQSFVKVHSKE--TFCDCKMLCOYSNCTF 93
QY 65 SLKLANIVERYSFPFLDAILNARRAAPCOAH-DKVKLFCLTDRLALCFCDPEPALHEQ 123
DB 94 NLVLEKIVKIKLPL-----LKGHPQCAEHGENLKLFSKPEGMICFOCKDARLS--- 144
QY 124 QVTGIDDAFDELQRELKDQALQDSEREHTEALQLLKROLAETKSKSLRTTIGEAF-- 181
DB 145 -----MGQSKDFLQ-ISEAVRFFTELAIQSOLQTLTKELQSLRTIQKDAIS 191
QY 182 -----PERLHRLRERQKAMLELEADTARTLTLDIQKVQYSQQLRKV 225
DB 192 AYKDNKIQLOONLSLEFLKHLQHFHNKEKIDLNDLRDEGKLLNEEMEVNLQEOCLVA 251
QY 226 QEGAQILQELAEADTRHTFTAGVASISERL-KG--KIHETNLTYEDPTTSKYTGPIQYTI 282
DB 252 KDLMTATQARMEQONSDFLTDITKLTIESMEKGMKTIIVPRLQIAKLSLGRFKGPIQYII 311
QY 283 WKSIFQDIHVPVPAALTDGTAHQRLTLDSDCTIVAGNLHPQLQDSPKRFDEVSVLG 342
DB 312 WKEMQAILSPGSQLTLDPKTAHNLVLSKTSQTSVCHCDV-KQVLDPDPERLSSVAVLG 370
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QY 343 SEAFSSGVHYWVWVAEKTQWVIGLAHEAASRKSQIQPSRGFYCI VMHDGNQYSACTE 402
DB 371 SKGFTSGKWYWEIEVGKTKTWIGVVRSEIIRKSGCPLTPEQGFLLRLNRNTDLKALDL 430
QY 403 PWTRLNVRDKLQKGVFLDYDQGLLIFYNADMSMLYTFREKFPKGLCSYFSPGQSHANG 462
DB 431 PRRSLTGLD-LRRVGVLDYEGGQVSYFNATTMTHTLTYTSSVFOEKLFPYLCPCLND-GG 488
QY 463 KNVQPLRI 470
DB 489 ENKEPLHI 496

RESULT 13
Q810I2 PRELIMINARY; PRT; 483 AA.
AC Q810I2;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ucla C., Meria G., Meroni G., Raymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081947; AAL91070.1; --
DR GO; GO:0005622; C-intracellular; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR00315; Znf_Ebox.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 483 AA; 54607 MW; DA3A7234CIA8145B CRC64;

Query Match 23.7%; Score 593; DB 11; Length 483;
Best Local Similarity 30.4%; Pred. No. 7.3e-32;
Matches 145; Conservative 83; Mismatches 217; Indels 32; Gaps 10;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRRCCITEHHVVRQEAQAGDCEPCRRRTFAEPALAP 64
DB 10 LQDLQCPICLVFEPLMLQCGHSYCKDCLDN--LSQHLDSLELCCPCRCQSVDCSSPP 67
QY 65 SLKLANIVERYSFPFLDAILNARRAAPCOAH-DKVKLFCLTDRLALCFCDPEPALHEQ 122
DB 68 NVSLARVI-----DALFPGDIPTVCVHRNPLSLFCEKQDBFCGLGGLGSHQ 119
QY 123 HQVTGIDDAFDELQRELKDQALQDSEREHTEALQLLKROLAETKSKSLRTTIGEAF 182
DB 120 HRVTPSVTVSRMKEELAGRISELKEHRNVEEHIGKLVNRRTRIINESDVFSVIRREF 179
QY 183 ERLHRLRERQKAMLELEADTARTLTLDIQKVQYSQQLRKVQEGAIILQERLAETDRH 242
DB 180 QELHHLVDEEKARCLEGLEHTRGLVASLDMQLEQAQGTQERLAQAEOVL-EQFGNSHH 238
QY 243 TELA--GVASLSRELKGIHETNLTYEDFTSKYTGPIQYTIWKSFLPDHPVPAALTD 300
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Db 239 EFIRFHSVASRAEVQOARPLEGVFSPISFKPALHQADIKLTVKWLFRKVLPAASLKLD 298
QY 301 PCTAHQRLILSDCTIVAGNLHPQLQSPKRFDEVSIVLGEAFSSGVHYWVVAEK 360
Db 299 PATAHPLLELSKGNIVVHCG-LLAQRASQPERFDYSTCVLASKGFSWGRHYWVVGSK 357
QY 361 TOWVIGLAHEAASRKSGSIQIOPSRGFCYCIWMDGNOYSACTBPWTRLNVRDKLVGVFL 420
Db 358 SDWRLGVIKGTASRGKLNKSPHGVWLLGLKEGRVYFAFGCPRLPLPVAGHPHRIQVYL 417
QY 421 DYDQGLLIFYNA---DDMSWLYTFREKPPGKL-----CSYFSPGOSHANGKNVQPL 468
Db 418 HYEQELTFDADRPDDLTLTYFOADFQGLYPILDTCT-----WHERGNSLPM 467

RESULT 14
Q81011
ID Q81011 PRELIMINARY; PRT; 483 AA.
AC Q81011;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Ucla C., Merla G., Meroni G., Reymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081950; AAL91073.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 483 AA; 54719 MW; 2C9171E12902AEAB CRC64;

Query Match 23.5%; Score 588; DB 11; Length 483;
Best Local Similarity 30.2%; Pred. No. 1.6e-31;
Matches 147; Conservative 81; Mismatches 207; Indels 52; Gaps 11;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCRITTEHWVQEAQAGDCPECRRTFAEPALAP 64
Db 10 LQDQLQPCICLVKPEKPLMLQCGHSYCKNCLDS--LSEHLDSLELRCPCVQSDVCSSSPP 67
QY 65 SLKLANIVERSYSPFLDAI-LNARRAAPCOAH-DKVKLFCLTDRALLCFPCDEPALHEQ 122
Db 68 NVSLARVI-----DALRLPGTEPTVCVHHNPLSLFCEKQDEFTICGLLGSQH 119
QY 123 HQVTGIDDAFDELQELKDQALQDSEREHTEALQLKROLATKSTKSLRTTIGFAF 182
Db 120 HRVTPVSTVSRMKELEADTARTLTIDEQVQRYSQLRKVQEGAGIQLERLAETDR- 179
QY 183 ERLHLLERQKAMLELEADTARTLTIDEQVQRYSQLRKVQEGAGIQLERLAETDR- 241
Db 180 QELHLLVDEEKARCLEGVESHTRGLVASLDMQL-----EQAGTQERLAQAERY 228
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QY 242 -----HTFLA--GVASLSERLKGKIHTNLITYEDPTTSKYTPLOYYTIWKSILFQDI 290
Db 229 LEQFNGESHEFIRFHSITSRGEVQOARPLEGVFSPISFKPALHQADIKLTVKWLFRKV 288
QY 291 HVPAAALTDPCGTAHQRLILSDCTIVAGNLHPQLQSPKRFDEVSIVLGEAFSSGV 350
Db 289 LEAPESLKLDPATAHPLLELSKGNIVVHCG-LLAQRASQPERFDYSTCVLASKGFSWGR 347
QY 351 HYWVVAEKTOWVIGLAHEAASRKSGSIQIOPSRGFCYCIWMDGNOYSACTBPWTRLNVR 410
Db 348 HYWVVGSKSDWRLGVIKGTASRGKLNKSPHGVWLLGLKEGRVYFAFGCPRLPLVA 407
QY 411 DKLDKVGVLFDYDQGLLIFYNA---DDMSWLYTFREKPPGKL-----CSYFSPGOSHAN 461
Db 408 GHPRIGVLYHYEQELTFDADRPDDLTLTYFOADFQGLYPILDTCT-----WHER 460
QY 462 GKNVQPL 468
Db 461 GNSLPM 467

RESULT 15
Q865W2
ID Q865W2 PRELIMINARY; PRT; 486 AA.
AC Q865W2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tripartite motif protein 50.
GN TRIM50.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RA Ucla C., Merla G., Meroni G., Reymond A.;
RT "Novel genes in the Williams-Beuren Syndrome critical region.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY081951; AAL91074.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001870; B302.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY receptor.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 486 AA; 54775 MW; A33ABD06EFC7A7F1 CRC64;

Query Match 23.2%; Score 581; DB 6; Length 486;
Best Local Similarity 29.4%; Pred. No. 4.7e-31;
Matches 141; Conservative 82; Mismatches 220; Indels 36; Gaps 10;

QY 5 LKDELLCSICLSIYQDPVSLGCEHYFCRCRITTEHWVQEAQAGDCPECRRTFAEPALAP 64
Db 10 LQDQLQPCICLVKPEKPLMLQCGHSYCKNCLDS--LSEHLDSLELRCPCVQSDVCSSSPP 67
QY 65 SLKLANIVERSYSPFLDAI-LNARRAAPCOAH-DKVKLFCLTDRALLCFPCDEPALHEQ 123
Db 68 NVSLARVIALQ-----LPGDPEPQVCTHHRNPLSLFCEKQDEFTICGLLGSQH 120
QY 124 QVTGIDDAFDELQELKDQALQDSEREHTEALQLKROLATKSTKSLRTTIGFAF 183
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Db 121 RVTPVSTVSRMKELEALISDLKQEQKVEQVAKLVNNRTRIYNESDVFSWIRREFQ 180
QY 184 RIHRLRRERQKAMLEBELEADTARTITDIEQKVQRYSQQLRKVQE---GAQILQERLAETD 240
Db 181 ELHHLVDEEKARCLEGVGHTRGVLVASLDMQL---EQARGAQERLAQATCMLEQFGNES 236
QY 241 RHTFLA--GVASLSERLKGKIHETNLTYEDPFTSKYTGPELOYTIWKSIFQDHPVPAALT 298
Db 237 HYEFTIRYHSTASSAELOQARLLEGAFSPISFKPLHQADIKLTVWKRJFRKVLPAPESLK 296
QY 299 LDPEGTARHORLILSDDCITIVAYGNLHPQPLQDQPKRPFDEVSVLGSEAFSSGVHYWEVVVA 358
Db 297 LDPTTAHPLLELSKGNVTVOCG-LLAQRASQPERDYSTCVLASRGFSCGRHYWEVVVG 355
QY 359 EXTQWVIGLAHEAARKGSIQIQPSRGFYCIWHDGNQYSACTEPWTRLNVRDKLDKGVV 418
Db 356 SKSDWRLGVIKGTASRKGLNKSPHGVWLI GLKEGRVYEAFSCPRVPLPVAGHPHRIGV 415
QY 419 FLDYDQGLLIFVNA---DDMSWLYTFREKFPQKL-----CSYFSPGQSHANGKNVQPL 468
Db 416 YLHYEQGELTFFDADRPDDLRLLYTFQADFQKLYPILDTC-----WHERGSNSLPM 467

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Job time : 44 secs